STIC-Biotech/ChemLib

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Hutzell, Paula

Sent:

Thursday, April 15, 2004 11:11 AM

To:

Graser, Jennifer; STIC-Biotech/ChemLib

Subject:

RE: rush search

approved

-----Original Message-----

From:

Graser, Jennifer

Sent:

Thursday, April 15, 2004 10:03 AM

To:

Hutzell, Paula rush search

Subject: rush: Importance: High

Hi Paula,

Could you please authorize the following rush search for an amendment which is due?

Thanks, Jennifer

STIC:

Please search SEQ ID NOs: 1; 1 (101-1176); 2; 3; 4; 5; 6; 6 (101-853); 6 (853-1176) from **10/608,504** in pending and commercial databases. They are species of one another and I need all of them searched.

Thanks, Jennifer Graser REMSEN EO3 B09/ 3C18 mailbox AU 1645 272-0858

Searcher: P. Schvebt
Phone: 272-25 26
Location: Reser E0 (A6)
Date Picked Up: Date Completed: 4 | 20
Searcher Prep/Review: 5
Clerical: Online time: 10

TYPE OF SEARCH:

NA Sequences: 7

AA Sequences: 2

Structures:

Bibliographic:

Litigation:

Full text:

Patent Family:

Other:

VENDOR/COST (where applic.)

STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.: Co up page
WWW/Internet:
Other (specify):



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor Remsen Bldg. 01 D86 571-272-2507

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> I am an examiner in Workgroup: Example: 1610
> Relevant prior art found, search results used as follows:
☐ 102 rejection
☐ 103 rejection
☐ Cited as being of interest.
Helped examiner better understand the invention.
Helped examiner better understand the state of the art in their technology.
Types of relevant prior art found:
☐ Foreign Patent(s)
 Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
> Relevant prior art not found:
Results verified the lack of relevant prior art (helped determine patentability).
Results were not useful in determining patentability or understanding the invention.
Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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	COMMENT	MEDLINE	JOURNAL	7777			AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	RESULT 1 AQ936633
Center for Genomics Research Karolinska Institute 17177 Stockholm, Sweden Tel: +46-8-728-6372 Fax: +46-8-337983	Contact: Podowski RM	20175728 10710430	Nucleic Acids Res. 28 (7), 1635-1639 (2000)	Wahlestedt, C.	Li,J., Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and	Xie,L., Muravenko,O.V., Kozyrev,S., Petrenko,L., Skobeleva,N.,	Zabarovsky, E.R., Gizatullin, R., Podowski, R.M., Zabarovska, V.V.,	1 (bases 1 to 473)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)	GSS.	AQ936633.1 GI:7213011	equence. AQ936633	ω	413

Result No.

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Match Length DB

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Description

SUMMARIES

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AQ936633 BX356664 BX376097 BX381961

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RESULT 2
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@flietech.com |
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DI015CA02NP1.
Location/Qualifiers
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                                                                                                                                              l Similarity
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NotI site.
                                                                                                                                                                                                                                                                                                                  /clone="CSODI015YB03"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
gimest. Five prime end enriched, double-strand cDNA was
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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68; Mismatches
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, 1 (Dases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2866.f
Contact: Feng Liang Email: fliang@lifetech.com URL:
Contact: Feng Liang Email: fliang@lifetech.com URL:
Chtp://fulllength.invitrogen.com/ InVitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSUDC022BG06QP1.
Location/Qualifiers
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BX376097 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo
CDNA clone CSODC022YM12 5-PRIME, mRNA sequence.
BX376097
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                                       TTNTTTNKTTTNMATKKKNTNKKKCNCKMKKKANKMMCNNNCKKKTKTKKKANKKANKMMKN
                                                                              TICGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAAATTAAGGGCCTC 652
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/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/clone_Tibt strand cDNA was primed with a NotI-oligo(dT)
/note="1st strand cDNA was primed, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECGR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                        3.3%; Score 41.8; DB 13;
9.1%; Pred. No. 2.7;
ive 238; Mismatches 310;
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                                                                                                          Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO72CCO3NP1.
Location/Qualifiers
                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hor

(Dases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                               BX381961

BX381961 Homo sapiens PLACENTA COT 25-NORMALIZED Clone CS0DI072YF05 3-PRIME, mRNA sequence.
                                                                                                                                                                                                Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
                                                    mol_type="mRNA"

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                                                                                    organism="Homo sapiens"
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                                          one="CS0DI072YF05"
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                                                                                                                                                                                                                                               GACCATCCGGTACTTCTTCGGGAAAGGCTGCTAAATGACAACTGATTTCTCCTGTATT
                                                                                                                                                                                                                                                                                                                                              TCTTGTGGTAATTCCAGGTCAGGCCCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTT
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MMNBKCVMKVKMKMCCKKVMMBKMCAKKKK
                                            ATCCTTAAGCCCCTACGTGAATCACAATTT
                                                                                                    MMKKUMMMBKKUCMMKKMCCMMKKKKHKKUMMKKOMMCKKBMMCKKUKMMIKMMVKKKKKA
                                                                                                                                              CTCCTTGTTGTCGCAGTATGTGCAGTCATTACTTTTGCGCTCCGGGCGGTTCCGTTCTTA
                                                                                                                                                                                                   KKCMCMKBMMCKMCMKMCMBKKNMMMMMMKMKMMMNKNKAMMKKDNMMMMMCAMMCM
                                                                                                                                                                                                                                                                                                 KKANNNNKANNNNNNNNNNNNKKMKMSKCKKKKMCCKMCCMCKKKKMBKGKMVCMCKMMKN
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BX540413
BX540413 AGENAE Gal
gallus cDNA clone g
BX540413
INRA, UMR INRA-ENSAR Genetique Animale 65, rue de Saint-Brieuc, RENNES cedex, Tel: +33 (0) 2.23.48.54.63
                                                                                                      Klopp,C. and Douaire,M. Construction and primary characterization multi-tissue cDNA libraries
                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                           Unpublished (2003)
Contact: Douaire M
                                                                                                                                                                      1 (bases 1 to 692)
Herault, F., Le Meuth-Metzinger, V., Desert, C.,
                                                                                                                                                                                                                                                                                 Gallus gallus
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AGENAE Gallus gallus multi-tissues library (
DNA clone gcab0001b.d.10 5prim, mRNA sequence
                                                                                                                                                                                                                                                                                                   (chicken)
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                                                                                                                                 chicken
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                           FRANCE
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(gcab) Gallus
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RESULT 6
AJ397466/c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae, Gallus.

1 (bases 1 to 718)
1 (bases 1 to 718)
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Plate: 0001 row: d column:
Seq primer: M13R.
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Email: Madeleine.Douaire@roazhon.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ397466 718 bṛ
AJ397466 dkfz426 Gallus gallus
AJ397466 71:7130433
EST. Gallus gallus (chicken)
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A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                              Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
                                                                                                                                                                                                                                                          Contact: Buerstedde JM
Cellular Immunology
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/db_xref="taxon:9031"
/clone="gcab0001b.d.10"
/tisue_type="adipose tissue, granulosa, multi-tissues, oviduct, small folicule, utero-vaginal gland"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pT7T3D-pac; Clone distribution : AGENAE Resource centre. Francois FIUMI, Francois.Piumi.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Gallus gallus"
/tissue type="Bursa of Fabricius"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
                                                                                                                       /organism="Gallus gallus"
/mol_type="mRNA"
                                                               /clone="2i7r1"
                                                                            /mol_type="mRNA"
/strain="CB"
/db_xref="taxon:9031"
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cDNA clone 2i7r1, mRNA sequence.
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1 (bases 1 to 743)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., clitek,R.W., Nunberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics Unpublished (2002)
Other_GSSs: OGUAX55TV
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CC684922
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OGUAX55TH ZM_0.7_1.5_KB Zea mays
genomic survey sequence.
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                                                                                                                                                                                  82;
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Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays
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                                TCGAGTTCGCCCTTTGCTCTCTCTTTGTCACGC 683
                                                          GTTTCGCGGCGGCCACCCGGATCCAGCTCGGCTTCGCGAGCGCCTCTAAAGCTTCAGGTC
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ACGAGAGGGCGCTTTGCTCTCTCCCTGTCCCGC
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ilarity 53.6%;
Conservative
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/db_xref="taxxon:4577"
/db_xref="taxxon:4577"
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/clone_lib="ZM_0.7_1.5_XB"
/note="Vector: pBCSK.; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                   organism="Zea mays"
mol_type="genomic DNA"
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Gallus gallus (chicken)

Gallus gallus

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel

Archosauria, Aves, Neognathae, Galliformes, Phasianidae,

Phasianinae, Gallus.

1 (bases 1 to 756)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbb

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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603211326F1 CSEQRBN13 Gallus
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CNS009WA 787 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR20K04 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simon Hubbard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="CEEQRBN13"
/clone_lib="CEEQRBN13"
/clone="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
/constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 928-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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/lab_host="DH10B"
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/clone="ChEST191c7"
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|strain="Layer"
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s cDNA clone ChEST191c7 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila bad, the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 CTACTTCGTCCTTTCSTCTTTMGTTGTAAMXWGKMWCTTGGAATCCKCTKYAGARARAAC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 TAATTTCGCCATATGGTTATATCGGATTTTTTTTTATTGGTCCGCTGA 168
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AL054013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
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Direct Submission
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EX425603 Homo sapiens NEUROBLASTOMA Homo
CLOBBO22ZA07 3-PRIME, mRNA sequence.
EX425603
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Verte
Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 885)
1 (W.B., Gruber, C., Jessee, J. and Polayes, D.
1 (J. W.B., Gruber, C.) Albraries and normalization
Unpublished (2001)
                                                                                                                                                                                                            BX425603.1 GI:30770486
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Conservative 15;
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/mol_type="genomic DNA"
/db_xref="texon:722"
/clone="BACR20K04"
/clone lib="RPCI-98"
/note="end : T7"
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                                                                                              Craniata; Vertebrata; I Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                  linear EST 15-MAY-2003 sapiens cDNA clone
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ALO60428
ALO60428.1 GI:4943359
GSS.
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BP 191 91006 EVRY cedex - France
Email: seqret@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/InVitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBBO22ZAO7FF1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Genoscope
                                                                                                                                                            Drosophila melanogaster genome sur BACR12G04 of RPCI-98 library from fly), genomic survey sequence.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                                                                                CNSOOSNG
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/clone_Tib="Homo saplens NEUROBLASTONA"
/clone_Telefone saplens NEUROBLASTONA"
/note="Vector: pc(MVSPORT 6; 1st strand cDNA was primed
/note="Vector: convSPORT 6; 1st strand cDNA was digested with Not I and cloned
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL0BB022ZA07"
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Pred. No. 11;
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survey sequence TET3 end of BAC #
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1076 CCGTTGCGATTACAGTGGTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  872
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                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 859)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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BP 191 91006 EVRY cedex - FRANCE (E-mail ; segref@genoscope.cns.f:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscop
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1 (bases 1 to 995)
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5', mRNA semienze
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                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
            ODNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution information Clone distribution information cound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGCTGGCACCATCGTTTTTGTTTGGACTGGTGAATCTTTTCTA 1178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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|mol_type="genomic DNA"
|db_xref="taxon:7227"
|clone="baCR12G04"
|clone="baCR12G04"
|clone_lib="RPCI-98"
|note="end : TET3"
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Pred. No. 12;
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IMAGE: 4149244 EST 22-NOV-2000

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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Piecer de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Plate: LLAM9410 row:
High quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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    genomic survey sequence.

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/tissue_type="glioblastoma with EGFR amplification"
/table to the "DH108 (T1 phage-resistant)"
/clone_lib="MCI_CGAP_Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Average insert size 1.5
/organism="Drosophila melanogaster"
                                                              Location/Qualifiers
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Query Match
Best Local Similarity
Matches 34; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope_sequence ID: CS0DI079DG08NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BX361080 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Faraday Avenue Genoscope sequence
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Genoscope
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       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="baCR19D16"
/clone=lib="RFCI-98"
/note="end: TET3"
                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="raxon:9606"
/clone="CSODIO79YN16"
/tissute_type="placeNTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PlaceNTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PlaceNTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
/mote="Ist strand cDNA was primed, double-strand cDNA was
primer. Five prime and enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                    3.0%;
   5%; Score 38.6; I
5%; Pred. No. 22;
147; Mismatches
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Pred. No.
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RESULT 13 CNS0091P

DEFINITION

CNS0091P

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792

ORIGIN

Best Loca Matches Query Match

90;

Local

REFERENCE AUTHORS TITLE

JOURNAL

SOURCE ORGANISM KEYWORDS VERSION ACCESSION

COMMENT

FEATURES

source

Gaps

9

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RESULT 15
CB657749
LOCUS
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AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                       Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Bo
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CB657749
835 bp mRNA linear EST 09-APR-20
OSJNEC13F02.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEc13F02 5', mRNA sequence.
CB657749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazus Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G. Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 835)
                                                                                                                                                                                                                                                                    BACKWARD: gga aac agc tat gac cat g
Plate: 13 row: F column: 02
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Rod Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDDMMMMMMMMMMMXMDKKKKKNDKKMMKKAKKKKKKKKKKKKKKKKKKMKKAMKKAMAKKK 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKKKKKKCCCCBKBCCCCKYKCCKBKKYCCYKCKKKKKCKKKYCCCBCCCKKKCBCYCC 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTGTGGGCGCAGCGCCCTGGGCGCCATCGCGCACATTGCTGGTGAACTTCCGC 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATACGGCTACGAATGGTGGGCA 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACGIATICIATGCGTTTTCATT 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KOLDINADADAMKKKKOHKOMKKKKKKKKONMKKKKKONMKKKKOKENAIKONAIKOKKKKKOADADAIKK 1064
                                                                            /organism="Oryza sativa (japonica cultivar-group)"

"mol type="mRNA"

"cultivar="Nipponbare"

/db xref="taxon:39947"

/clone="0SJNEG13F02"

/tissue_type="Leaf"

/dev stage="3 week"

/lab_host="DH10B"
                 /clone lib="OSJNEc"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
/hoI; 6 hrs after innoculation with Rice Blast (C9240-1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Box 210088, Tucson, AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhou, B., Mazur, E.,
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Best Local S
Matches 89
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                                                                                                            79
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                                                      ATGCCGCCGGGTGTTCGACCGGATCGCGCACCCCGACCTGCCGGCCTGGAACGCGCTGCT
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                                                                                                                                                                 Conservative
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Pred. No. 28;
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                                                                                                                                                                   Gaps
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Search completed: April 17, 2004, 20:01:40 Job time : 4123.78 secs

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Title:
Perfect score;
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Kennerknecht, N., Sahm, H., Eggeling, L. and Pfefferle, W.

Nucleotide sequences coding for the export of branched cacids, process for the isolation thereof and use thereof patent: US 6613545-A 6 02-SEP-2003;

Location/Qualifiers
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CCCACTGTTTTCCCGGCCTGATTTTCGCGGGGCTCCACCGAAATGCTGGTCATCGCCCTCGT
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Best Local Similarity
Matches 1271; Conserv
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Degussa AG (DE) / FORSCHUNGSZENTRUM JUELICH GMBH (DE) Location/Qualifiers
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Query Match
Best Local Similarity
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Location/Qualifiers
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Kennerukunehito,N., Sahm,H., Eggering,L. and Pfefferle,W. Nucleotide sequence encoding the discharge of branched ammethod of isolating the same and utilization thereof patent: DEGUSSA HUBLIS AC, PORSCHUNGSZENTRUM JUBLICH GMBH OS Corynebacterium glutamicum ATCC14752
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27-OCT-1999 DE 19951708.8
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Direct Submission

Submitted (24-WAY-2002) Satoshi Nakagawa, Kyowa Hakko Kogyo Co.

Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida,

Tokyo 194-8533, Japan (E-mail:snakagawa@xanagen.com,

Tel:81-44-829-3031, Fax:81-44-813-1651)

This sequence is conducted by collaboration of Kyowa Hakko Kogyo

Co. Ltd. And Kitasato University.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum ATCC 13032
Corynebacterium glutamicum ATCC 13032
Bacteria, Actinobacteria, Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Corynebacterium glutamicum ATCC 13032 DNA,
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                                                                                         /gene="Cg10001"
/note="PF00308:Bacterial dnaA protein
/note="PF00308:Chromosomal replication
/codon start=1
/transT table=11
/product="ATPase involved in
/protein id="BAB97394.1"
/db_xref="GI:21322765"
                                                                                                                                                 'gene="Cgl0001"
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                                                                                                                                                                                                                                                                     ATCC 13032"
                                                                                                    initiator
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2292. .3476

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="TIGR00611:recf: RecF
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PF00986:DNA gyrase B subunit, carboxyl terminus
PF01751:Toprim domain
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TIGR01058:parE_Gpos: DNA topoisomerase IV,
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                CCTATTIGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACCATCCGGTACTTCTTCTTGGG
                                                     TTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTTGTGGTAATTCCAGGTCAGGC
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/protein_id="BAB97403.1"
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regulator (lrp) genes, complete
Ar454053
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1 (bases 1 to 2105)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Export of L-isoleucine from Corynebacterium glutamicum: two-gene-encoded member of a new translocator family J. Bacteriol. 184 (14), 3947-3956 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Juelich
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Kennerknecht, N., Eggeling, L. and Sahm, H.
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1538. .1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid export protein"
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                                                                                                                                                                                                                                                                                                                                                                                       complement (708.
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                                                                                                                                         /trānblation="moktoeihsslevspskaalbeddkgvrryeiaoglktslaagl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="LIV-E transporter component
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acid export protein"
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AEGIILGYSADIHPAVMNRGFEVTVDVTLSNFDRSTVDNFESSVAQHDEVLELHRLFG
SPDYFVRIGVADLEAYEQFLSSHIQTVPGIAKISSRFAMKVVKPARPQV"
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/protein_id="AAM46687.1"
/db_xref="GI:21311382"
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                           ATGCTGGTCATCGCCCTCGTTGTGGGCGCGCAGCGCCCTGGGCGCCATCGCGCTCACCACA
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                                                                                                                                                                                                                                                                                                                 /organism="unknown"
/mol_type="genomic"
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Patent: EP 1108790-A 289 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
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    GCTGCAGGTTTGGGCATGTACCCCGATTGGTATTGCGTTTTGGTCTCTTGGTTATTCAATAC
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/db_xref="taxon:1718"
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Degussa AG (DE) ; FORSCHUNGSZENTRUM JUELICH GMBH (DE) LOCALION/Qualifiers
                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum
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Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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SYWVFGGLTGVAIABLIPFBIKGLEFALCSLFVTLTLDSCRTKKQIPSLLLAGLSFTI
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RIGIN	
Query Mato Best Local Matches	<pre>%atch 59.2%; Score 753; DB 6; Length 753; scal Similarity 100.0%; Pred. No. 3.3e-196; s 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>
য	101 GTGCAAAAAAGCGCAAGAGTTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG 160
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ř	61 GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT 120
¥	221 GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC 280
ਰੱ	121 GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTTGGTTTGTTT
¥	281 GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGGCCTGATTTTCGCGGGCTCCACCGAA 340
ъ	181 GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCCGGCCTGATTTTCGCGGGCTCCACCGAA 240
γ	341 ATGCTGGTCATCGCCCTCGTTGTGGGGGCAAGCGCCCCTGGGGGCCCATCGCGCTCACCACA 400
p	241 ATGCTGGTCATCGCCTTGTTGTGGGCGCAGCGCCCTGGGCGCCATCGCGCTCACCACA 300
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8	361 AACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT 420
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ф	421 GCGGCCAGGCCGCAGGCTGGTCGGCGACTTATCTCAATGCAAATAGCGTTTCAC 480
γ	581 TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTGCTTTTGAA 640
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P.	601 CGAACGAAAAGCAGATCCCTTCTCTGCTGCTGCTGGCAGGTTTGAGCTTCACCATTGCTCTT 660
ঠ	761 GTGGTAAITCCAGGTCAGGCCCTATTTGCGGCCGCTGGTGATCTTCTTGGGTCTGTTGACC 820
дb	AGGTCAGGCCCTATTTGC
γ	821 ATCCGGTACTTCTTTGGGAAAGGCTGCTAAA 853
Вb	721 ATCCGGTACTTCTTGGGAAAGGCTGCTAAA 753

BD014992

Nucleotide sequence encode method of isolating the BB014992

BD014992.1 GI:22555799

JP 2001169788-A/2.
unidentified
unclassified. 753 encoding the same bp DNA linear PAT 27-AUG-2002 the discharge of branched amino acid, and utilization thereof.

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REFERENCE
AUTHORS
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OS Corynebacterium glutamicum ATCC14752
PN JP 2001169788-A/2
PD 26-JUN-2001
PF 24-CCT-2000 JP 2000324315
PR 27-CCT-1999 DE 19951708.8
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C C12N15/00,
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                                                                                                                               GCGGCCAGGCCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC
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                                                       ATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCTGC
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Location/Qualifiers
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NOVEL DOLYNUCIOCIÓN.

PATENT: JP 2002191370-A 289 09-JUL-2002;

KYOWA HAKKO KOGYO CO LTD

OS COTYNEBACTETIUM Glutamicum

PM JP 2002191370-A/289

PD 09-JUL-2002

PP 15-DEC-2000 JP 2000405096

PI SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEI

PI KEIKO OCHIAI,

PI HARUHIKO YOKOI, NAOKO TATEISHI, AKIHIRO
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Nakagawa, S., Mizoguchi, H., Ando, S.,
Yokoi, H., Tateishi, N., Senoo, A., Ik
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GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGGCTCCACCGAA
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                                                                        GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC
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SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI,
KEIKO OCHIAI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HARUHIKO YOKOI, NAOKO TATEISHI, AKIHIRO SENOO, MASATO IKEDA, AKIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="unidentified'
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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    Hayashi, M., Ochi
Ikeda, M. and Ozaki,

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3.3e-196;
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, 64	Qy 3	Query Mat Best Loca Matches	AUTHORS TITLS TOURNAL PEATURES SOURCE SOURCE ORIGIN	RESULT 15 AX137083/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy 8	Qy 7 Db 6	Qy 7	Db 6	Qу 5 Дъ 4	Qy 5	Оу 4 Дъ 3	Qy 4 Db 3	Qy 3.	Дb 1
69 AAACTACCCGGCAATTGTGTGATGATTGTAGTGTGCAAAAAACGCAAGAGATTCATTC	9 AATGGAATCTAGCTTCATATATTGCACAATAGCCTAGTTGAGGTGCGCAAACTGGCAACA 68 	ch 28.8%; Score 365.6; DB 6; Length 397; 11 Similarity 98.9%; Pred. No. 2e-89; 368; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Moeckel, B., Pfefferle, W., Puehler, A., Kalinowski, J. and Bathe, B. Nucleotide sequences coding for the lrp gene Patent: Ep 1090993-A 7 11-APR-2001; Degussa AG (DE) Location/Qualifiers 1. 397 /organism="Corynebacterium glutamicum" /mol_type="unassigned DNA" /db_xref="texaon:1718" /note="lrp-Teil l"	AXI37083 Sequence 7 from Patent EP1090993. AXI37083 AXI37083.1 GI:14273428 Corynebacterium glutamicum Corynebacterium glutamicum Bacteria; Actinobacteria; Actinobacteria; Actinobacteria; Actinobacteria; Corynebacterineae; Coryneae; Corynebacterineae; Corynebacterineae; Corynebacterineae; Corynebacterineae; Corynebacterineae; Corynebacterineae; Corynebacterineae; Coryneae; Corynebacterineae; Coryneae;	21 ATCCGGTACTTCTTCGGAAAGGCTGCTAAA 853 	61 GTGGTAATTCCAGGTCAGGCCCTATTTGCGGCGCCTGCTGATCTTCTTGGGTCTGTTGACC 820	01 CGAACGAAAAAGCAGATCCCTTCTCTGCTGCTGCTGCAGGTTTGAGCTTCACCATTGCTCTT 760	41 ATTAAGGGCCTCGAGTTCGCCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCTGC 700	81 TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA 640	21 GCGGCCAGGCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC 580	61 AACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT 520	401 TIGCIGGIGAACTICCGCCACGIAIICTAIGCGIITTCAITCCCGCIGCAIGIGGICAAA 460 	341 ATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCCTGGGCGCCATCGCGCTCACCACA 400	.81 GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAA 240

	CACGCCCCCGGG		당 성
	CARCGCCCTGG 380	369	5
CATCGCCCTCGTTGTGC	FITTCCGGCCTGATTTTCGCGGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCG	76	밁
TCATCGCCCTCGTTGTGC	TTTCCGGCCTGATTTTCGCGGGCTCCAACGAAATGCTGGTCATCGCCCTCGTTGTGGGCG	309	Ş
AATGGTGGGCAGCCCCAC	GTATTGCGTTTGGTCTCTTGGTTATTCAATACGGCTACGAATGGTGGGCAGCCCCACTGT	136	90
HAATGGTGGGCAGCCCCAC	GTATTGCGTTTGGTCTCTTGGTTATTCAATACGGCTACGAATGGTGGGCAGCCCCACTGT	249	Ś
GGTTTGGGCATGTACCCGA	ACGAAATCGCGCAAGGTCTAAAAAACCTCCCTTGCTGCAGGTTTTGGGCATGTACCCGATTG	196	밁
GGTTTGGGCATGTACCCGA	ACGAAATCGCGCAAAGGTCTAAAAAACCTCCCTTGCTGCAGGTTTGGGCATGTTACCCGATTG	189	5
GATGATAAAGGTTATCGGC	S GCCTGGAGGTGTCGCCATCCAAGGCAGCCCTGGAACCAGATGATAAAGGTTATCGGCGCT	256	밁
GATGATAAAGGTTATCGGC	CCTGGAGGTGTGCCATCCAAGGCAGCCCTGGAACCAGATGATAAAGGTTATCGGCGCT	129	8
		316	B

Search completed: April 19, 2004, 18:29:50 Job time : 5394 secs

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Aaq36952	AAQ36952	N	19012	2.8	36.2	45	
Adb13462	ADB13462	ø	751		36.4	44	a
Acc94996	ACC94996	7	751	2.9	36.4	43	ი
Abs58541	ABS58541	σ	751		36.4	42	ი
Ab194832	ABL94832	σ	751	2.9	36.4	41	a
Aas1001	AAS10011	ហ	751		36.4	40	a
Aca59269	ACA59269	ທ	751		36.4	9	ი
Aah84682	AAH84682	4	751	2.9	36.4	38	o
Aah02433	AAH02433	4.	751		36.4	37	ი
Aas63460	AAS63460	4	751		36.4	9	ი
Aah93368	AAH93368	4.	751		36.4	យ បា	ი
Abs71157	ABS71157	w	751		36.4	3. <u>4</u>	a
Aaa06252	AAA06252	ω	751	2.9	36.4	ω G	a
Aav61146	AAV61146	N	751		36.4	32	n
Aav58489	AAV58489	N	751		- 36.4	31	a
Aca42205	ACA42205	7	1230		36.8	30	
Ada71938	ADA71938	7	2000	2.9	37.2	29	
Abx66366	ABX66366	o	1024		37.2	28	
Ac£65382	ACF65382	7	243072		37.6	27	
Continuation	ACF67367_20	7	110000	_	37.6	26	
Aax84332	AAX84332	N	5059	3.0	37.6	25	ი
ACI69125	ACF69125	7	759	3.0		24	

ALIGNMENTS

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AAH2110 1
AAH2110 AAH2120
AAH2110 AAH220
AXX AAH22
AXX AAH22
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AXX L-am
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DR WILL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KW L-amino acid production; brnE; branched-chain amino acid;
KW coryneform bacterium; leucine; isoleucine; valine; medicine;
KW animal nutrition; ds.

XX Corynebacterium glutamicum.

XX Location/Qualifiers
FT CDS /*tag= a
FT /product= "brnF"
FT CDS /*tag= b
FT /*tag= b
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Claim 4 (i); Page 13; 23pp; German. New export genes from coryneform bacteria, useful for increasing fermentative production of branched-chain amino acids. WPI; 2001-391595/42. P-PSDB; AAB86247, AAB86248. Kennerknecht N, Eggeling L, 11-CCT-2000; 2000EP-00122057. (DEGS) DEGUSSA AG. (KERJ) FORSCHUNGSZENTRUM.JUELICH GMBH. 99DE-01051708. Sahm H, Pfefferle W;

27-OCT-1999;

02-MAY-2001.

This invention describes a novel isolated polynucleotide (I) containing

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cc at least one sequence that (i) is 70% identical with a sequence that cc encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) cor (5); (iii) encodes a polypeptide at least 70% identical with (3) cc or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least 70% identical with (3) cc or 50%; (iii) is the complement of (i) or (ii), or (iv) contains at least 70% or 50%; (iii) is the complement of (i) or (iv) contains at least 70% or 50%; (iii) is the complement of (i), or (iv) contains at least 70% or 50%; (iii) is the complement of (iv) or 324 bp (4); (b) cc coryneform microorganisms, especially Corynebacterium, transformed with 70% or or more (I), where these are replicative DNA; (c) production of 20% or or more (I), where these are replicative DNA; (c) production of 50% or expecially overexpressed; and (d) method for isolating the brnE and/or 60% or production of production of or isolating the brnE and/or 60% or genes. (I) is used for transformation of coryneform bacteria being 60% or equivalent sequences) are amplified, 60% or equivalent sequences) are amplified. 60% or equivalent sequences and or settle brnE and/or 60% or fermentative production of branched-chain amino acids, 60% or equivalent sequences. 60% or expectifically leucine, isolation of branched-chain amino acids. 60% or isolation of branched-chain amino acids. 60% or isolation of branched-chain amino acids. 60% or isolation of the invention 60% or isolation 60% or isolatio
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Best Local Similarity 100.
Matches 1271; Conservative
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                  100.0%; Score 1271;
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tive 0; Mismatches
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standard; DNA; 1271

ВP

(first entry)

L-amino acid production; brnF; brnE; branched-chain amino ac coryneform bacterium; leucine; isoleucine; valine; medicine;

Corynebacterium glutamicum Location/Qualifiers

2000EP-00122057

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This invention describes a novel isolated polynuclsotide (I) containing containing at least one sequence that (i) is 70% identical with a sequence that (containing the process at least one of 251 amino acid (aa) (3) or 108 aa (5) (2) polypeptides; (ii) encodes a polypeptide at least 70% identical with (3) (2) or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least 70% identical with (3) (2) protein derived from sequences of 753 bp (2) or 324 bp (4); (b) (2) protein derived from sequences of 753 bp (2) or 324 bp (4); (b) (2) coryneform microorganisms, especially Corynebacterium, transformed with (2) one or more (I), where these are replicative DNA; (c) production of (2) one or more (I), where these are replicative DNA; (c) production of (contain L-aa by fermentation of coryneform bacteria in which the contained-chain in the contained contained the bring of the for termsforms and (d) method for isolating the bring of bring genes. (I) is used for transformation of coryneform bacteria being contained for fermentative production of branched-chain amino acids, sequences for isolation. (I) can also be used as source of primers and contained and animal nutrition. (I) can also be used as source of primers and contained process of the isolation of related sequences. Transformation with (I) contained the corynebacterium glutamicum ATCC 13032 bring and bring procesins described in the contained contained the corynebacterium glutamicum ATCC 13032 bring and bring procesins described in the contained contained the corynebacterium described in the contained contained contained the corynebacterium described in the contained contained contained the contained c
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Best Local Similarity 100
Matches 1271; Conservative
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(KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH
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TTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACTGCGGCCAGGCCAGGCTG
                                                                                              CGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAAACCCCATTGCCCGTTTCTA
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            Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
                                                                                                                                                                                                                                           C glutamicum coding sequence fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                             26-SEP-2001
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                                        EP1108790-A2
                                                                                                    Corynebacterium glutamicum
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(first entry)

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CCGCATGCCCTCAATTTGAAGGGGATGCGGATTTTTTTAAGGAACCTAGAAAAGGCTTAAG	1201	δ
GGCACCATCGTTTTTGTTGGACTGGTGAATCTTTTCTAAAACTGCATAATAACAAAAA	1141	βģ
GGCACCATCGTTTTTGTTGGACTGGTGAATCTTTTCTAAAACTGCATAAATAA	1141	Ş
GCGATTACAGTGGTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCT	1081	문
GCGATTACAGTGGTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCT	1081	Ş
TCAACGTTTCGCAGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTT	1021	뮍
TCAACGTTTCGCAGCAATGCGATAGATCTGAAGACCTCTAACCTTTGGTCTCATTGCCGTT	1021	Ş
CAATTTGTGGCAAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCA	961	문
CARTTTGTGGGCAAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCA	961	Ş
GTCATTACTTTTGCGCTCCGGGCGGTTCCGTTCTTAATCCTTAAGCCCCCTACGTGAATCA	901	문
GTCATTACTTTTGCGCTCCGGGCGGTTCCTTAATCCTTAAGCCCCTACGTGAATCA	901	ş
AAAGGCTGCTAAATGACAACTGATTTCTCCTGTATTCTCCTTGTTGTCGCAGTATGTGCA	841	문
AAAGGCTGCTAAATGACAACTGATTTCTCCTGTATTCTCCTTGTTGTTGTCGCAGTATGTGCA	841	δ
CCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACCATCCGGTACTTCTTCTTGGG	781	용
CCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACCATCCGGTACTTCTTCTTGGG	781	Ŋ
TTCTCTGCTGCAGGTTTGAGCTTCACCATTGCTCTTGTGGTAATTCCAGGTCAGGC	721	용
TTCTCTGCTGCTGCAGGTTTGAGCTTCACCATTGCTCTTGTGGTAATTCCAGGTCAGGC	721	Ş
CCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCTGCCGAACGAA	661	F
CCTTTGCTCTCTCTTTGTCACGCTGACTTTGGATTCCTGCCGAAACGAAAAAGCAGATCCC	661	¥
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TCTCACCGGAGTGGCGATCGCAGAGTTGATTCGTTTTTGAAAATTAAGGGCCTCGAGTTCGC	601	¥.
GTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCACTCCTACTGGGTATTCGGCGG	541	퓻
GTCGGCGTGGCGACTTATCTCAATGCAATAGCGTTTCACTCCTACTGGGTATTCGGCGG	541	¥
TTCGGTTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACTGCGGCCAGGCCCGCAGGCTG	481	ŏ

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  TTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACTGCGGCCAGGCCCAGGCTG
                                            CGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAAACCCCATTGCCCGTTTCTA
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Senoh A, Ikeda M,
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L-amino acid production; brnF; coryneform bacterium; leucine;

brnE; branched-chain amino isoleucine; valine; medicir

acid;

nutrition; ds.

Corynebacterium glutamicum

AAH21110

standard;

DNA; 753

βP

05-SEP-2001

(first entry)

glutamicum

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This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that (c) encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) co or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least (c) or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least (c) for consecutive bases from (i)-(iii). The invention also describes (a) coryneform microorganisms, especially Corynebacterium, transformed with one or more (I), where these are replicative DNA; (c) production of coryneform bacteria in which the brnB and/or brnF genes (or equivalent sequences) are amplified, (c) especially overexpressed; and (d) method for isolating the brnB and/or brnF genes (or equivalent sequences) are amplified, (c) used for fermentative production of branched-chain amino acids. (c) used for fermentative production of branched-chain amino acids. (c) used for isolatino of coryneform bacteria being used for isolatino isolation of primers and conditionally leucine, isolation of branched-chain amino acids. (d) probes for isolation of branched-chain amino acids. (e) probes for isolation of branched-chain amino acids. (f) contained by the production of branched-chain amino acids. (f) contained by the probacterium glutamicum ATCC 14752 brnF protein described in the method of the invention
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AACCCCATTGCCCGTTTCTATTCGGTTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT
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100.0%; Pred. No. 1.3e-230;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 C; 194 G; 208 T; 0 U; 0 Other;
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07-APR-2000;
03-AUG-2000;
The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino
                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakagawa
Tateishi
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2000JP-00159162.
2000JP-00280988.
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Senoh A, Ikeda M,
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Ozaki A;
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                                                                                                                                                                                                                                                                                                                                         TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA
                                                                 standard;
                                                                                                                                ATCCGGTACTTCTTCTTGGGAAAGGCTGCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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               (first
                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.2%;
100.0%;
                                                                  564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 753; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>,</u>
                                                                  뭐
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
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This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to corynebacterium glutamicum, particularly for monitoring a fermentation process to determine expression levels of Ç. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                       \ddot{\mathbf{0}}
                                                                                                                                                                                                                                                                                                                                                                  DE10128510-A1
                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                 Coryneform;
                                                                                                                                                                  New nucleic acid array useful for Corynebacterium glutamicum during from Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                             13-JUN-2001; 2001DE-01028510
                                                                                                                                                                                                                                                                                                                   13-JUN-2001;
                                                                                                                                                                                                                                                                                                                                           19-DEC-
                                                                                                                                                                                                                                             Farwick M,
                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                    (DEGS )
                                                                                                                                                                                                                                                                                                                                                                                                                                        glutamicum derived ORF
                                                                                                                                                                                                                      2003-279970/28
                                                                                                                                               Page 647;
                                                                                                                                                                                                                                                                                                                    200108-01028510
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                                                                                                                                                                                                                                                                                                                                                                                          glutamicum.
                                                                                                                                               709pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                  acid
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                                                                                                                                                                                                                                                                                                                                                                                                                     fermentation;
                                                                                                                                                                                   monitoring mRi
fermentation,
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                                                                                                                                                                                                                                                Bathe
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                                                                                                                                                                                    mRNA expression
on, comprising n
                                                                                                                                                                                                                                                                                                                                                                                                                     culture;
                                                                                                                                                                                                                                                 Huthmacher
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                                                                                                                                                                                     nucleic
                                                                                                                                                                                                 e
E
                                                                                                                                                                                       acid
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Query Match Best Local Sequence Local Similarity hes 564; Conserv 564 BP; 91 A; 167 43.5%; Ç Score Pred. 0; Mis 144 core 553; DB red. No. 1.8e Mismatches .. O 162 DB 7; 1 Ή. 0 u; o Length Other;

0

Indels

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Gaps

δ 밁 5 片 밁 S 밁 Ş 밁 8 밁 289 120 409 349 300 589 240 529 180 469 709 360 649 19 \vdash GAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAAACCCCAT CATCGCCCTCGTTGTGGGCGCAAGCGCCCCTGGGCGCCATCGCGCTCACCACATTGCTGGT ATGGTGGGCAGCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGT ATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGT GCCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCACTCCTACTG GAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAAACCCCAT ĠĠŦĀŦŦĊĠĠĊĠĠŦĊŦĊĀĊĊĠĠĀĠŦĠĠĊĠĀŦĊĠĊĀĠĀĠŦŶĠĀŦŦŶĊĊŦŤŦŦĠĀĀĀŤŦĀĀĠĠĠ GGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAAATTAAGGG gecegeaggergeregecergeceaerrarereaargeaaaragecerrreaereeraerg rececerriciariceerriricecectrareeaceaaeceracecaercaereaecae TGCCCGTTTCTATTCGGTTTTTCGCGCCTTATCGACGAAGCCTACGCAGTCACTGCGGCCAG AAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTTGTGGTAAT ccrceaerreeccerriecrererriereaeecreaerreearreecarreecaaceaa Conservative 119 768 419 359 648 299 588 239 528 179 468 408 9

420

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RESULT 7
AARF61693/c
AAF61693;
XX
AC AAF61693;
XX
AC AAF61693;
XX
DT 12-JUL-2001 (first entry)
XX
DE C. glutamicum lrp encoding DNF
XX
DE C. glutamicum lrp encoding DNF
XX
C. glutamicum lrp encoding DNF
XX
Permentation; L-amino acid pro
XX
Corynebacterium glutamicum.
XX
PN Fermentation; 2000EP-00121159.
XX
COCYNEBACTERIUM glutamicum.
XX
PN EP1090993-A1.
XX
PN EP1090993-A1.
XX
COS-OCT-1999; 99DE-01047792.
XX
PN (DEGS) DEGUSSA-HUELS AG.
XX
PN (DEGS) DEGUSSA-HUELS AG.
XX
PN (DEGS) DEGUSSA-HUELS AG.
XX
PN (DEGS) PROFERENCE W, Puel
XX
PN (DEGS) PROFERENCE N, PUEL
XX
PN (DE
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                                                                                                                                                                                                                                                                                                                                           Matches 368;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel isolated nucleic acid (I) from coryneform bacteria used for the fermentative production of selected L-amino acids, by fermenting the amino acid-producing coryneform in which at least the lrg gene has been weakened or amplified, then isolating amino acids that have accumulated in the medium or cells. (I) is used to transform coryneforms for production of L-amino acids, specifically lysine and isolating, which are used in medicine and particularly as animal feed supplement. It may also be used as probes and primers for isolating related sequences. Regulating expression of (I) improves production of amino acids, especially of L-lysine. This sequence encodes a fragment of the Corynebacterium glutamicum lrp protein which is used in the method described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 397 BP; 96 A; 100 C; 104 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 16; 22pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New lrp gene from coryneform bacteria, used to prepare transformants with increased synthesis of amino acids, particularly lysine and isoleucine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-2000; 2000EP-00121159
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                                   129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTCTTCTTGGGAAAGGCTGCTAAA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTCTTCTTGGGAAAGGCTGCTAAA 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCAGGTCAGGCCCTATTTGCGGCCGCTGCTGATCTTCTTGGGTCTGTTGACCATCCGGTA
GCCTGGAGGTGTCGCCATCCAAGGCAGCCTGGAACCAGATGATAAAGGTTATCGGCGCT
                                                                                                                                                                                                                   AATGGAATCTAGCTTCATATATTGCACAATAGCCTAGTTGAGGTGCGCAAACTGGCAACA
                                                                                              AATGGAATCTAGCTTCATATATTGCACAATAGCCTAGTTGAGGTGCGCAAACTGGCAACA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ion; L-amino acid production; lrp gene; lysine; isoleucine,
animal feed supplement; ds.
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99DE-01047792.
                                                                                                                                                                                                                                                                                                                                                                  28.8%;
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                                                                                                                                                                                                                                                                                                                                        Score 365.6; DB 4;
Pred. No. 2.2e-106;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         쁌
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                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                                                                                                                                                                                   Length
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AATGGAATCTAGCTTCATATATTGCACAATAGCCTAGTTGAGGTGCGCAAACTGGCAACA

Query Match Best Local (Matches

Similarity

28.8%; Score 365.6; DB 4; 98.9%; Pred. No. 3.2e-106;

4

Indels Length

0

Gaps

0

83

Conservative

o •

Sequence 778 BP; 175 A; 208 C; 207 G; 188 T; 0 U; 0 Other;

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RESULT 8
AAP61695/c
ID AAP61695;
XX AAF61695;
XX AAF61695;
XX AAF61695;
XX Permentat
XX Corynebac
XX Corynebac
XX Corynebac
XX Permentat
XX Permentat
XX Dilatan
XX Dilatan
XX Dilatan
XX Noeckel B
XX WPI; 2001
XX W
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                                                        This invention describes a novel isolated nucleic acid (I) from coryneform bacteria used for the fermentative production of selected L-amino acids, by fermenting the amino acid-producing coryneform in which at least the lry gene has been weakened or amplified, then isolating amino acids that have accumulated in the medium or cells. (I) is used to transform coryneforms for production of L-amino acids, specifically lysine and isolaucine, which are used in medicine and particularly as animal feed supplement. It may also be used as probes and primers for isolating related sequences. Regulating expression of (I) improves production of amino acids, especially of L-lysine. This sequence encodes a fragment of the Corynebacterium glutamicum lrp protein which is used in the method described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1090993-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fermentation; L-amino acid production; lrp gene; lysine; isoleucine;
medicine; animal feed supplement; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 17; 22pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New lrp gene from coryneform increased synthesis of amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. glutamicum lrp encoding DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76
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This invention describes a novel isolated polynuclectide (I) containing at least one sequence that (i) is 70% identical with a sequence that encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) polypeptides; (ii) encodes a polypeptide at least 70% identical with (3) or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least 15 consecutive bases from (i)-(iii). The invention also describes (a) protein derived from sequences of 753 bp (2) or 324 bp (4); (b) coryneform microorganisms, especially Corynebacterium, transformed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L-amino acid production; brnF; brnE; branched-chain amino acid; coryneform bacterium; leucine; isoleucine; valine; medicine; animal nutrition; ds.
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FORSCHUNGSZENTRUM JUELICH
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                                                                                                                                                                                                                                                                                coryneform bacteria, useful for increasing on of branched-chain amino acids.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            one or more (1), where these are replicative DNA; (c) production of branched-chain L-aa by fermentation of coryneform bacteria in which the brnE and/or brnF genes (or equivalent sequences) are amplified, especially overexpressed; and (d) method for isolating the brnF genes. (I) is used for transformation of coryneform bacteria being used for fermentative production of branched-chain amino acids, specifically leucine, isoleucine and valine, which are useful in medicine and animal nutrition. (I) can also be used as source of primers and probes for isolation of related sequences. Transformation with (I) increases yield of branched-chain amino acids. This sequence encodes the Corynebacterium glutamicum ATCC 14752 brnE protein described in the method of the invention
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 TTTGTTGGACTGGTGAATCTTTTC 324
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RESULT 10
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07-APR-2000;
03-AUG-2000;
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Nakagawa Tateishi

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Mizoguchi H, Ando S, Hayashi Senoh A, Ikeda M, Ozaki A;

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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                               Corynebacterium
                                                                                                                              Coryneform; nucleic acid array;
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                                                                                                                                                                                               04-JUN-2003
                                                                                                                                                                                                                                                             ACA01970 standard; DNA; 324 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 324 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID NO 290; 246pp + Sequence Listing; English
13-JUN-2001; 2001DE-01028510
                                 19-DEC-2002
                                                                                                                                                              glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                           1093
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DB; AAG90036.
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                                                                                                                                                                                                                                                                                                                                                                         TTTGTTGGACTGGTGAATCTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                              GTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTG 1092
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                                                                                                                                                                                                                                                                                                                                             TTTGTTGGACTGGTGAATCTTTTC
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                                                                                                                                                                                               (first entry)
                                                                                                                                                              derived
                                                                                               glutamicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.5%; Pre
                                                                                                                                                              ORF SEQ ID 1961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 324; DB 5;
Pred. No. 4.4e-9;
0; Mismatches
                                                                                                                                fermentation;
                                                                                                                                                                                                                                                                                                                                                                            1176
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hes 0;
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Key -35_signal

Location/Qualifiers 62. .67

Fermentation; L-amino medicine; animal feed

acid production; supplement; ds.

lrp gene;

lysine; isoleucine;

Corynebacterium

glutamicum

12-JUL-2001

(first entry) lrp encoding

glutamicum

DNA.

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ARESULT 12
AAF61688/c
ID AAF61688;
XX AAF61688;
XX AAF61688;
XX T2-JUL-200
XX C. glutami
XX Fermentati
XX Fermedicine;
XX M medicine;
XX XX Fermedicine;
XX Fe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to corynebacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA0010. ACA02188 represent C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid array useful for Corynebacterium glutamicum during from Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUN-2001; 2001DE-01028510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 324 BP; 60 A; 79 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glutamicum derived polynucleotides described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 647; 709pp; German
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                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA; 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTGTTGGACTGGTGAATCTTTTC 1176
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Pred. No.
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 185
                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel isolated nucleic acid (I) from coryneform bacteria used for the fermentative production of selected L-amino acids, by fermenting the amino acid-producing coryneform in which at least the 1rp gene has been weakened or amplified, then isolating amino acids that have accumulated in the medium or cells. (I) is used transform coryneforms for production of L-amino acids, specifically lysine and isolencine, which are used in medicine and particularly as animal feed supplement. It may also be used as probes and primers for isolating related sequences. Regulating expression of (I) improves production of amino acids, especially of L-lysine. This sequence encode the Corynebacterium glucamicum lrp protein which is used in the method described in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 14-15; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New lrp gene from coryneform bacteria, used to prepare transformants with increased synthesis of amino acids, particularly lysine and isoleucine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -10_signal
                                        04-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DEGS )
                                                                  ACA01968
                                                                                          ACA01968 standard; DNA; 177
             glutamicum
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                                                                                                                                                                                 TCGGC 185
                                                                                                                                                                                                                                                                                 TGGCAACAAAACTACCCGGCAATTGTGTGTGATGATTGTAGTGTGCAAAAAAACGCAAGAGAT
                                                                                                                                                                                                                                     TCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTGGAACCAGATGATAAAGGTTA 180
                                                                                                                                                                                                                                                              TGGCAACAAAACTACCCGGCAATTGTGTGATGATTGTAGTGTGCAAAAAAACGCAAGAGAT
                                                                                                                                                           TCGGC 1
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                                        (first entry)
                derived ORF
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EP1108790-A2 Corynebacterium organic acid

20-JUN-2001

18-DEC-2000; 2000EP-00127688

Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

fragment SEQ ID NO: 3408

synthesis;

ds.

glutamicum.

C glutamicum coding sequence

26-SEP-2001 AAH68373;

(first entry)

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RESULT 14
AAH68373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid array useful for Corynebacterium glutamicum during from Corynebacterium glutamicum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUN-2001; 2001DE-01028510
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177; Conserv
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Pred. No.
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is an uncleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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Tateishi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
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318; Conserv
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 TCAAAAATAACAAGGATTATTCGCTGCCATTATTCGCGGTGGTATTGGCTCTGGTTTCCG
                                GCCGAACGAAAAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTC
                                                                                                                                                                                                 CAGCCCCCCCCCGCGATATCAGTGGCACGCGGGTGCTTACCGTTCAAATTTTGTGCC
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                                                                                                AAATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTTGGATTCCT
                                                                                                                               AAGCTCTGTGGGTTATCCCAGGAATTÁTTGGCGCCTTGGTTGGTCAAGTGCTGCCCGATG
                                                                                                                                                               <u>ACTCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTG</u>
                                                                                                                                                                                                                                 CGGCCAGGCCGCAGGCTGGTCGGCGTG---GCGACTTATCTCAATGCAAATAGCGTTTC
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2000JP-00159162.
2000JP-00280988.
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Senoh A,
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Ikeda M,
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Pred. No. 9e-30
0; Mismatches
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Ozaki A;
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Best Local :
                                                                                                                                                                                                                                                     Corynebacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
                                                                                                                                                                                                                     Sequence 711
                                                                                                                                                                                                                                                                                                                                              This invention describes a novel nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid array useful for Corynebacterium glutamicum during from Corynebacterium glutamicum.
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Qy 819 CCATCCGGTACTTCTTC 835	Oy 759 TIGIGGIAATICCAGGICAGGCCCTATITGCGGCGCTGCIGATCTICTIGGGTCTGITGA 818 Db 593 GITTIGIGGCGCCCGAGCAGAIGCIGGITATCGCITIGACCACGIACTITITGAICCTIC 652	Qy 699 GCCGAACGAAAAAGCAGATCCCTTCTCTGCTGCTGCAGGTTTGAGCTTCACCATTGCTC 758	Qy 639 AAATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTTGTCACGCTGACTTTGGATTCCT 698	Qy 579 ACTCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGGAGAGTTGATTCCTTTTG 638	Oy 522 CGGCCAGGCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTC 578	Qy 462 ACCCCATTGCCCGTTTCTATTCGGTTTTTCGCGCTTATCGAAGGCTACGCGAGTCACTG 521	Db 233 TCATGGTGAATTTCGGCGACATTTTCTACGGTCTACCTTCCCACGCCACGCATCAAGT 292

Search completed: April 19, 2004, 11:41:56 Job time: 595.9 secs

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US-09-252-991A-2761

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Sequence 3205, Ap
Sequence 2761, Ap
Sequence 17, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 16656, A
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APPLICANT: KENNERGNECHT, NICOLE
APPLICANT: SAHM, HERWANN
APPLICANT: SAEM, HERWANN
APPLICANT: SGGELING, LOTHAR
APPLICANT: PFEFERLE, WALTER
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: LSOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/265496/MAS
CURRENT FALING DATE: 1999-112-23
PRIOR APPLICATION NUMBER: US/09/471,803A
CURRENT FILING DATE: 1999-112-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR RETING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
Matches 1271; Conserv
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LOCATION: (101)...(853)
OTHER INFORMATION: brnF
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ORGANISM: Corynebacterium glutamicum
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                                                                            CCGCATGCCCTCAATTTGAAGGGGATGCGGATTTTTTAAGGAACCTAGAAAAGGCTTAAG 1260
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TYPE: DNA

TYPE: DNA

CORANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: gene
LOCATION: (101)...(853)
COTHER INFORMATION: brnF
NAME/KEY: gene
LOCATION: (853)...(1176)
COTHER INFORMATION: brnE
COCATION: 853)...(1176)
COTHER INFORMATION: ATCC13032
US-09-471-803A-6

100.0%: Scor-
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APPLICANT: KENNERKNECHT, NICOLE

APPLICANT: SAHM, HERMANN

APPLICANT: SAHM, HERMANN

APPLICANT: SGGELING, LOTHAR

APPLICANT: BEGGELING, LOTHAR

APPLICANT: PFEFFERLE, WALTER

TITLE OF INVENTION: NUCLECTIDE SEQUENCE CODING FOR THE EXPORT OF

TITLE OF INVENTION: SEAUCHED CHAIN AMINO ACIDS, PROCESS FOR THE

TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF

FILE REFERENCE: 21123/265496/MAS

CURRENT APPLICATION NUMBER: US/09/471,803A

CURRENT FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: DE 199 51 708.8

PRIOR FILING DATE: 1999-10-27

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1

SOFTWARE: Patentin Ver. 2.1
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US-09-471-803A-6
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APPLICANT: KENNERGYECHT, NICOLE
APPLICANT: SAHM, HERMANN
APPLICANT: SAHM, HERMANN
APPLICANT: BEGGELING, LOTHAR
APPLICANT: PFEFFERLE, WALTER
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: 1SOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/265496/MAS
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR FILING DATE: 1999-10-27
                                                                                                                                                                                                                                                                                                        RESULT 3
US-09-471-803A-2
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GENERAL INFORMATION:
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; SOFTWARE; PATENTIN Ver. 2.1
; SEQ ID NO 2
; LENGTH: 753
TYPE: DNA
ORGANISM: Corynebacterium glutamicum FEATURE:
INAME/KEY: CDS
LOCATION: (1)..(753)
OTHER INFORMATION: BOTHER OF STATEMENT OF STATEME
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US-09-471-803A-4
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               US/09471803A
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APPLICANT: EGGELING, LOTHAR
APPLICANT: PERFERLE, WALTER
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/265496/MAS
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1399-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 3016
LENGTH: 756
TYPE: DNA
                                                                                                                                                 Sequence 3016, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2004001
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OTHER INFORMATION: brnE
OTHER INFORMATION: ATCC14752
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; ORGANISM: Klebsiella pneumoniae US-09-489-039A-3016
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US-08-232-463-14
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5670367
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-DOS/MS-DOS
SOFTWARE: PATENTIAN NUMBER: US/08/232,463
                               TELEFAX: (703)683-4105
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                 APPLICATION NUMBER: US/07/93:
FILING DATE:
APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite
                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SCHEIFLINGER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1800 Dia
CITY: Alexandria
            TYPE: nucleic acid
 STRANDEDNESS:
                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCATTATTTACGCCGCCGCCAGCCAGTTTGTGATCACCGCCATGTTGGCCGCCGGCAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTCATTCC 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCTGATTTTCGCGGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COTTTGGTCTCTTGGTTATTCAATACGGCTACGAATGGTGGGCAGCCCCACTGTTTTCCG
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                                                                                                    (703)836-9300
(703)683-4109
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single
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52.2%;
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                                                                                                                                                           30472/114 IMMU
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Pred. No. 3.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                Version #1.
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25
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linear

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RESULT 7
US-09-107-532A-1266
US-09-107-532A-1266
, Sequence 1266, Application US/09107532A
; Patent No. 658275
; GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
APPLICANT: Lynn A DOUCETTE ACID
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Best Local
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ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                            FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1410
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MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                              CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                560 TCAATGCAAATAGCGTTTCACTCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  620 GCAGAGTTGATTCCTTTTGAAATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTC
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                                                                                                                                                                                              APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                               OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                             CITY: Waltham
                                                                                                                                                                                                                             SOFTWARE: ASC
                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 221; Mismatches
                                                                                                                                                                                                                APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                02354
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Pred. No. 2e-
                                                                                                                                                                                                                                                                                                                                                                                                                                       and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUT
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                                                                                                                                                                                                                                                                                                                                                                                            CORPORATION
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Sequence 11376, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 11376

LENGTH: 1038

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa
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LOCATION: (B) LOCATION 1...768;
SEQUENCE DESCRIPTION: SEQ ID NO: 1266;
US-09-107-532A-1266
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327
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                                                                                                                                                                                                                                                                                                                                             l Similarity
77; Conserv
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Pred. No. 0.0072;
                                                                                                                                                                                                                                                                                                                                             Score 39.2; DB Pred. No. 0.014; O; Mismatches
       448
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US-09-252-991A-11418
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US-09-621
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GENERAL INFORMATION: Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 107196.136
PTILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-621-976-8976
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LENGTH: 1086
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Best Local (
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ORGANISM: Pseudomonas aeruginosa
-09-252-991A-11418
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Best Local &
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SOFTWARE: Patent.pm
SEQ ID NO 8976
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
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APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human
                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 39
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Local Similarity 12.6%;
nes 30; Conservative 11
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Similarity 55.0%;
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Pred. No. 0.0086;
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                                                                                                                               RESULT 12
US-09-252-991A-3205/c
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FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION UNDEBR: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: PSECENT.pm
SEQ ID NO 18033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18033, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
Sequence 3205, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND P
TITLE OF INVENTION: AERUGINOSA FOR DIA FILE REFERENCE: 107196.136
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Best Local :
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les 49; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               522 CGGCCAGGCCCGCAGGCTGGTCGGCGACTTATCTCAATGCAAATAGCGTTTCACT
                                                                                                                                                                                                                                                                              253 MMYKGGRMYWWWRGGMWKRMYWMYKKKSMWKGSCMWKRAWWARKTTYYTWAWYYTTYYKR
                                                                                                                                                                                                                                                                                                                 762 TGGTAATTCCAGGTCAGGCCCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACCA
                                                                                                                                                                                                         313 MCCYYMRKTTYCMMWYSRWWRGSMWTARGAWWMCYWWYY 352
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                                                                                                                                                                                                                                                                                                                                                                                         GAACGAAAAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTTG 761
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                                                                                                                                                                                                                                            TCCGGTACTTCTTCGGGAAAGGCTGCTAAATGACAACT 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 135; Mismatches 156;
     J. Rubenfield et al.
NN: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
NN: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
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Pred. No.
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                                              PSEUDOMONAS
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3205
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                                                                                                                                                                                                        US-09-020-956-12/c
                                                                                                                                                                                                                              RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 2761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 65; Conserv
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LENGTH: 1140
                                                                                                                                                            Sequence 12, Application US/09020956
Patent No. 6261562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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PRIOR TILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                               APPLICANT: Xu, Jiangchun APPLICANT: Dillin, Davin C. TITLE OF INVENTION: COMPOUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          1333
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                                                                                                                                             INFORMATION:
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                                                                                                                                                                                                                                                                                          GCCGCCCAGGCCGCACCTTCCTGGTCACCGCGCTGGTCTACTTCTGCTACG 1384
                                                                                                                                                                                                                                                                                                                                                                              TACTICCIGATCAACCICGGCGCCCTCGGCCGCTGATCGGCCTGACTCTCGGCGTC 1332
E: SEED and BERRY LLP 6300 Columbia Center,
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1998-02-18
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                                                                                 COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
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Pred. No. 0.097;
0; Mismatches 47; Indels
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  701 Fifth Avenue
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US-09-020-956-12
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Best Local (
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Patent No. 6262245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY MAKI, DAVID J.

NAME: MAKI, DAVID J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622,4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Jiar APPLICANT: Dillon, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                STREET: 6300 CITY: Seattle
                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 98104
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                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 25-FEB-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 TGGTGTACACCACAATGGCTGAGCACTTCCCTGACGT 314
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Database
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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1271
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|: /cgn2_6/ptodata/1/pubpna
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Copyright (c) 1993 - 2004 Compugen Ltd.
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2 6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
2 6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
2 6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2 6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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SUMMARIES

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ALIGNMENTS

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APPLICANT: EGGEING, LOTHAR
APPLICANT: PERFERLE, WALTER
APPLICANT: PERFERLE, WALTER
TITLE OF INVENTION: UCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
FILE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
CURRENT APPLICATION NUMBER: US/10/608,504
CURRENT APPLICATION NUMBER: US/9/471,803
PRIOR APPLICATION WHERE: US/9/471,803
PRIOR APPLICATION UNMER: US/9/471,803
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
US-10-608-504-1
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APPLICANT: KENNERKRECHT, NICOLE
APPLICANT: SAHM, HERMANN
APPLICANT: EGGELING, LOTHAR
APPLICANT: PFEFFERLE, WALTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10608504 Publication No. US20040014123A1
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LOCATION: (853)..(1176)
OTHER INFORMATION: brnE
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LOCATION: (101)..(853)
OTHER INFORMATION: brnF
                              OTHER INFORMATION: ATCC14752
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                                                                   CCGCATGCCCTCAATTTGAAGGGGATIGCGGATTTTTTAAGGAAACCCTAGAAAAAGGCTTAAG 1260
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RESULT 3
US-03-738-626-1
US-03-738-626-1
Sequence 1, Application US/09738626
Publication No. US2002019760SA1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NAVOSHI, MIKIRO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: OCHAI, KEIKO
APPLICANT: OCHAI, KEIKO
APPLICANT: OCHAI, KAIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
FILE REFERENCE: 249-125
FILE REPERENCE: 249-125
FILE REPERENCE: 129-12-16
PRIOR APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-16
PRIOR APPLICATION NUMBER: US/09/73484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: US/09/37484
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
JENGTH: 3309400
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

δ Query Match 100.0%; Score 1271; D Best Local Similarity 100.0%; Pred. No. 0; Matches 1271; Conservative 0; Mismatches 277149 276729 GCGCGATCAATGGAATCTAGCTTCATATATTGCACAATAGCCTAGTTGAGGTGCGCAAAC 276788 277029 276969 276849 276789 421 181 121 481 TICGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACTGCGGCCAGGCCCGCAGGCTG 61 1 GCGCGATCAATGGAATCTAGCTTCATATATTGCACAATÄGCCTAGTTGAGGTGCGCAAAAC TGTGGGCGCAGCGCCCCTGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTTTCCGCCA CCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTCGT TCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTTGCTGCAGGTTTTGGGCAIGTA 240 TCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTGGAACCAGATGATAAAGGTTA TGGCAACAAACTACCCGGCAATTGTGTGATGATTGTAGTGTGCAAAAAAACGCCAAGAGAT CGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAAAACCCCCATTGCCCGTTTCTA 480 TGTGGGCGCAGCGCCCTGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTTCCGCCA CCCACTGTTTTCCGGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTCGT CCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATACGGCTACGAATGGTGGGCAGC CCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATACGGCTACGAATGGTGGGCAGC 300 TCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTGGAACCAGATGATAAAGGTTA TGGCAACAAACTACCCGGCAATTGTGTGATGATTGTAGTGTGCAAAAAAACGCAAGAGAT 276848 DB 9; <u>,</u> Length 3309400; Indels 0; Gaps 540 420 360 180 120 277088 277208 277148 277028 276968 276908 60 0

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RESULT 4

US-09-738-626-289

Sequence 289, Application US/09738626

; Publication No. US20020197605A1

; GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI

APPLICANT: MIZOGUCHI, HIROSHI

APPLICANT: MIZOGUCHI, HIROSHI

APPLICANT: ANDO, SELKO

APPLICANT: OCHIAI, KEIKO

APPLICANT: OCHIAI, KEIKO

APPLICANT: YOKOI, HARUHIKO

APPLICANT: TATEISHI, NAOKO

APPLICANT: TATEISHI, NAOKO

APPLICANT: SENOH, AKIHIRO

APPLICANT: NENOH, AKIHIRO

APPLICANT: NENOH, AKIHIRO

APPLICANT: NENOH, AKIHIRO

APPLICANT: OZAKI, AKIO

ITILE OF INVENTION: NOVEL POLYNUCLEOTII
ANT: HAYASHI, MIKIRO
ANT: OCHIAI, KEIKO
CHIAI, KEIKO
ANT: YOKOI, HARUHIKO
ANT: TATEISHI, HAROKO
ANT: IXEDA, MASATO
ANT: IXEDA, MASATO
ANT: OZAKI, AKIO
DF INVENTION: NOVEL FOLYNUCLEOTIDES
SPERENCE: 249-125
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CCURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER: OF SEQ ID NOS: 7059
SOFTWARE: PatentIN ver. 3.0
SEQ ID NO 289
LENGTH: 753
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-289
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                                                          ATCCGGTACTTCTTCTTGGGAAAGGCTGCTAAA 853
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Sequence 2, Application US/10608504
; Publication No. US20040014123A1
; GENERAL INFORMATION:
APPLICANT: KENNERKAECHT, NICOLE
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
APPLICANT: EFFFERLE, MALTER
ITILE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF
ITILE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE
ITILE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
ITILE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
ITILE OF INVENTION NUMBER: US/10/608,504
CURRENT APPLICATION NUMBER: US 09/471,803
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 99/471,803
PRIOR APPLICATION NUMBER: US 199/471,803
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                         TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA
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RESULT 6
US-10-134-640-7/c
Sequence 7, Application US/10134640
Publication No. US20030017555A1
GENERAL INFORMATION:
APPLICANT: Bathe, Brigitte
APPLICANT: Workel, Jorn
APPLICANT: Workel, Bettina
APPLICANT: Pobler, Alfred
APPLICANT: Pfefferle, Walter
TITLE OF INVENTION: Nuclectide Sequences Coding for
FILE REFERENCE: 9901.09 BT
CURRENT APPLICATION NUMBER: US/10/134,640
CURRENT APPLICATION NUMBER: US/10/134,640
CURRENT FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 9
SOPTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 397
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: misc_feature
COCATION: (1): (397)
OTHER INFORMATION: 1rp part 1
US-10-134-640-7
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Best Local Similarity
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CAGCGCCCCTGG
                                                                   TTTCCGGCCTGATTTTCGCGGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCG
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                                                                                                           TTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCG
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Publication No. US20030017555A1
GEMERAL INFORMATION:
APPLICANT: Bathe, Brigitte
APPLICANT: Kalinowski, Jorn
APPLICANT: Publer, Alfred
APPLICANT: Publer, Alfred
APPLICANT: Prefferie, Walter
TITLE OF INVENTION: Nucleotide Sequences Coding for the 1rp Gene
FILE REFERENCE: 990109 BT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/134,640
CURRENT FILING DATE: 2002-04-30
NUMBER OF SEC ID NOS: 9
SOFTWARE: Patentin version 3.1
SEC ID NO 9
LENGTH: 778
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 368;
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Best Local
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NAME/KEY: misc feature

CONTION: (377)..(397)
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OTHER INFORMATION: upsream region of the lrp
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LOCATION: (434)...(778)
OTHER INFORMATION: downstream region of the lrp gene
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LOCATION: (398)..(433)
OTHER INFORMATION: 3'-region
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OTHER INFORMATION: 21 bp
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LOCATION: (350)..(376)
OTHER INFORMATION: 5'-region
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les 368; Conservative
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                                                                                      GTATTGCGTTTGGTCTCTTGGTTATTCAATACGGCTACGAATGGTGGGCAGCCCCACTGT
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                                                                  GTATTGCGTTTGGTCTTGGTTATTCAATACGGCTACGAATGGTGGGCAGCCCCACTGT
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                                   TTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCC
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Pred. No. 5.2e-113;
O; Mismatches 4;
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RESULT 9 US-10-608-504-4

Sequence 4, Application US/10608504
Publication No. US20040014123A1
GENERAL INFORMATION:
APPLICANT: KENNERKNECHT, NICOLE

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APPLICANT: HAVASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIKO
APPLICANT: SENOH, AKIHIKO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-125
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: J99/377484
PRIOR APPLICATION NUMBER: J99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOCTWARRE: PATENTIN OS: 7059
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US-09-738-626-290
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-290
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAVASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 290, Applic Publication No. US20 GENERAL INFORMATION:
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Best Local Similarity
Matches 324; Conserv
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                                          TTTGTTGGACTGGTGAATCTTTTC 1176
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ANDO, SEIKO
  TTTGTTGGACTGGTGAATCTTTTC 324
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5. US20020197605A1
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RESULT 10
US-10-134-640-1/c
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Best Local Similarity 100.
124; Conservative
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
FILE REFERENCE: 990109 BT
CURRENT APPLICATION NUMBER: US/10/134,640
CURRENT FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                           Sequence 1, Application US/10134640 Publication No. US20030017555A1
                                                                                                             APPLICANT: Bathe, Brigitte
APPLICANT: Kalinowski, Jorn
APPLICANT: Puhler, Alfred
APPLICANT: Mockel, Bettina
APPLICANT: Pfefferle, Walter
TITLE OF INVENTION: Nucleotide Sequences Coding for the 1rp Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: EGGELING, LOTHAR
APPLICANT: PFEFFERLE, WALTER
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 7601/80525
CURRENT APPLICATION NUMBER: US/10/608,504
CURRENT FILING DATE: 2003-06-30
PRIOR APPLICATION NUMBER: US 09/471,803
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR PILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-27
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LOCATION: (1)..(324)
OTHER INFORMATION: brnE
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ORGANISM: Corynebacterium glutamicum
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100.0%; Er/
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; NAME/KSY: -35 signal
; LOCATION: (62)..(67)
; OTHER INFORMATION:
US-10-134-640-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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APPLICANT: ANY COLLARY MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIDITO
APPLICANT: OZAKI, AKIDITO
APPLICANT: OZAKI, AKIDITO
CURRENT APPLICATION NUMEER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMEER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMEER: JP 00/159162
PRIOR APPLICATION NUMEER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 3408
LENGTH: 711
TYDE: DNA
                                                                         ORGANISM: Corynebacterium glutamicum US-09-738-626-3408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3408, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (151)..(612)
OTHER INFORMATION: 1rp-Gen
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ORGANISM: Corynebacterium glutamicum
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TGGCAACAAAACTACCCGGCAATTGTGTGATGATTGTAGTGTGCAAAAAACGCAAGAGAT 120
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10.0%;
Score 127.4; DB 9; Pred. No. 6.1e-32;
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APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILLING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILLING DATE: 1999-12-16
PRIOR PPLICATION NUMBER: JP 00/159162
PRIOR FILLING DATE: 2000-04-07
PRIOR FILLING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILLING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
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APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
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                                                                                                                                                                                                                              YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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REQUENCE 6067, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IXEDA, HARUO
APPLICANT: HORIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089

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RESULT 13
US-10-156-761-6067
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SEQ ID NO 1
LENGTH: 3309400
TYPE: DNA
ORGANISM: Corynebacterium
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Best Local Similarity
Matches 318; Conserv
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                                                              TICICCGCGICCGCTIC
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Conservative
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Pred. No. 1.4e-29;
0; Mismatches 296;
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; TYPE: DNA; ORGANISM: Streptomyces a; FEATURE: ; NAME/KEY: CDS; LOCATION: (1)..(594) US-10-156-761-6067
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US-10-156-761-1/c
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                                                                                                                                     ; FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (4187715)
; OTHER INFORMATION: a, t
US-10-156-761-1
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Matches
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PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6067
LENGTH: 594
                                                                    Query Match
Best Local S
Matches 103
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                                                                                                                                                                                                                        SEQ ID NO 1
LENGTH: 9025608
TYPE: DNA
ORGANISM: Streptomyces avermitilis
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                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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 7327430 TCACCGGCTGGGCGACGAGGTGCTCGGCATGGTGGTCGGCACCGCGCTCGGCTGGG 7327371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 TCACCGGCTGCGCCATCGGCGAGGTGCTCGGCATGGTGGTCGGCACCGCGCTCGGCTGGG
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HORIKAWA, HIROSHI
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50.7%;
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                                                                    Score 43; DB 1
Pred. No. 1.4;
0; Mismatches
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Pred. No. 0.0029;
0; Mismatches 100; Indels
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                                                                                                     DB 14; Length 9025608;
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; ORGANISM: Homo
US-10-184-644-80
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SEQ ID NO 80
LENGTH: 351
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Publication No. US20030044930A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 45; Conserv
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                      TT.YAC.ABBMC.B..SH.ASGNWYYNY..R.G...T..TCYYBSHKB..NYMGK.B.Y.
                                                                                                                                            B.S.S.TBCRT.NHSGCSW..C..SBCDBAYHGCGM...CSSGTYABT.TBCTSS.TRB. 111
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..CM.M.GA...S.SCBSS.MT.R.WNSTTTS.BT
                                    AACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCT
                                                                                                   TTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA 460
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Gurney, Austin L.
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ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AR391953	RESULT 1
acids, process for the isolation thereof and use thereof Patent: US 6613545-A 1 02-SEP-2003;	Nucleotide sequences coding for the export of branched chain amino	Kennerknecht, N., Sahm, H., Eggeling, L. and Pfefferle, W.	1 (bases 1 to 1271)	Unclassified.	Unknown.	Unknown.		AR391953.1 GI:40115724	AR391953	Sequence 1 from patent US 6613545.	AR391953 1271 bp DNA linear PAT 18-DEC-2003		

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Kennerknecht, N., Sahm, H., Eggeling, L. and Pfefferle, W.

Kennerknecht N., Sahm, H., Eggeling, L. and Pfefferle, W.

Nucleotide sequences coding for the export of branched chain

acids, process for the isolation thereof and use thereof

Patent: US 6613545-A 6 02-SEP-2003;

Location/Qualifiers
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ATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTTCCTGC
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                                                                                                     GCGGCCAGGCCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC
                                                                                                                                    AACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT
                                                                                                                                                    AACCCCATIGCCCGITTCTATICGGITTTCGCGCTTATCGACGAAGCCTACGCAGTCACT
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Mismatches 0;
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Length Indels

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18-DEC-2003

CDS	CDS	REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	AX137709 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM		\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$		B
/protein_id="CAC39923.1" /db_xref="GI:14273887" /db_xref="GI:14273887" /db_xref="REMTREMBL (CAC39923" /db_xref="REMTREMBL (CAC39923" /translation="MOKTORIHSSLEVSPSKAALEPDDKKGYRRYEIAQGLKTSLAAGL (translation="MOKTORIHSSLEVSPSKAALEPDDKKGYRRYEIAQGLKTSLAAGL (MYPIGIAPGLLVIQYGYEWWAAPLFSGLIFBGSTEMLVIALVVGAAPLGAIALTTLL VNFRHYFYAPSPLHVVKNPIAFFYSVFALIDEAYAVTAARPAGWSAWRLISMQIAFH SYWIFGGLIGVATAELIPPEIKGLEFALGLEVTLTLDSCRTKKQIPSLLLAGLSFTI ALVVIPGQALFAALLIFLGLLTIRYFFLGKAAK" 8531179 /note="unnamed protein product; brnE" /codon_start=1	/organism="Corynebacterium giutamicum" /mol_type="unassigned DNA" /mole="ATCC14752" /note="ATCC14752" 101856 /note="unnamed protein product; brnF" /codon_start=1 /trans1 table=11	Kennerknecht, N., E. Nucleotide sequenci proteins, method f. Patent: EP 1096010 Degussa AG (DE); Location/, 1, .1271	AX137709 Sequence 1 from Patent EP1096010. AX137709 AX137709.1 GI:14273886 Corynebacterium glutamicum Corynebacteria, Actinobacteridae, Actinomycetales;	CCTTGTTGAGCGTTGCCGTTGCGAFTACAGTGGTGGCGCAFCTTCTTGGCGGTCGACGCACCAFCTTTTGTTGAGCGGTTGACGCTTTCTTC 1076	841 TTAAGCCCCTACGTGAATCACAATTTGTGGGCAAAATGGCGATGTGGATGCCAGCAGGAA 900	21 TIGGTACTICTICGGAAAAGGCTGCTAAATGACTAATTGACTAATTCTCCTGTATTCTCCCTGTATTCTCCCCCCGTACTTCTCCTGTATTCTCCCCCCCC	641 ATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCTGC 700 601 CGAACGAAAAAGCAGATCCCTTCTCTGTGCTCGCAGGTTTGAGCTTCACCATTGCTCTT 660
821 781 881 841 941	Db 701 CGAACGAAAGAAGCAGATCCCTTCTGCTGCTGCTGAGCCTTGAGCTTTGAGCTCTTT 760 Qy 661 GTGGTAATTCCAGGTCAGGCCCTATTTGCGGGCTGCTGATCTTTGGGTCTGTTGACC 720	5 5 4 1 5 6 4 1 1 6 6 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	361 ARCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGAAGCCTACGCAGTCACT 42	pb 281 ddcthacdaarddftdddcaaccchactriticaddddcardarfttricaddddcardaa 340 Qy 241 ATGCTGGTCATCGCCCTCGTTGTGGGCGACCCCTGGGCCCACCACCACA 300	161 121 221 181	Query Match 100.0%; Score 1076; DB 6; Length 1271; Best Local Similarity 100.0%; Pred. No. 8.3e-275; Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG 60	/transl_table=11 /protein_id="CAC39924.1" /protein_id="CAC39924.1" /db_xref="GI:14273888" /db_xref="REPRIENBL:CAC39924" /translation="MITDFSCILLVVAVCAVITFALRAVPFLILKPLRESQFVGKMAM /MPRAGILAIUTASTFRSNAIDLKTLTFGLIAVAITVVAHLLGGRRTLLSVGAGTIVFV GLVNLF" ORIGIN

Conservative 0; CARARACCCARGAGATI CALLILLIA IIII	ORIGIN Query Match 100.0%; Score 1076; DB 6; Length 1271; Best Local Similarity 100.0%; Pred. No. 8.38-275;	/db_xref="remtrembl:cac39928" /translation="mttdpscillyvavcavitpalravpflilkplresopvgkmam /mpagilaliltastfrsnaidlktlffgliavaitvvahllogrrtllsvgagtivpv glynlp"	/codon_start=1 /transI_table=11 /protein_id="CAC39928.1" /db_xref="GI:14273895"	ALVVIPOALFAALLIPLOLLTIRYFFILOKAAK" CDS 8531179 /note="unnamed protein product; brnE"	/ OD_XZELE" KEMIKENDE I KANDEYSZEVALEPDDKGYRRYBIAQGLKTSLAAGL / LYBHOL AL ONE MOKTQEIKSZEVAKALEPDDKGYRRYBIAQGLKTSLAAGL / GMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPLGAIALTTLL / UNFRHYEYAFSFPLHVYKDFIARFYSVERALIDEAYAVTAARPAGWSAWELISMOIAFH / CHAMPOOL MOTELIA FETTINEETKALEFT FOR TOTTOTT TO KOTTEVALISMOIAFH	/ CURCHE BEASTER 1 / trans1 table=11 / protein id="CAC39927.1" / db_xref="CAC3994" / db_xref="CAC3994"	CDS /note="unnamed protein product; brnf"	source	proteins, method for isolating them and their use Patent: EP 1096010-A 6 02-MAY-2001; Degussa AG (DE); FORSCHUNGSZENTRUM JUELICH GMBH (DE) IOGATION (Onalifform	Corynebacterineae; Corynebacteriaceae; Corynebacterium. REFERENCE 1 AUTHORS Kennerknecht,N., Eggeling,L., Sahm,H. and Pfefferle,W. TITLE Nucleotide sequences coding for branched-chain amino acids export	Corynebacterium glu Corynebacterium glu Corynebacterium glu Bacteria; Actinobac	AX137714 LOCUS AX137714 DEFINITION Sequence 6 from Patent EP1096010. ACCESSION AX137714 VERSTON AX137714 VERSTON AX137714	SULT 4	1021 CCTTGTTGAGCGTTGGCGCTGGCACCATCGTTTTTGTTTG	961 CCTTIGG	Qy 901 TCCTTGCCATTTTGACCGCATCAACGTTTCGCAGCAATGCGATAGATCTGAAGACTCTAA 960
RESULT 5 BD014991 LOCUS DEFINITION Nucleotide sequence encoding the discharge of branched amino acid, method of isolating the same and utilization thereof. ACCESSION D014991 VERSION BD014991 UERSION BD014991 S014991.1 GI:22555798 KEYMORDS JP 2001169788-A/1. SOURCE unidentified	Qy 1021 CCTTGTTGAGCGTTGGCGCTGGCACCATCGTTTTTGTTGGACTGGTGAATCTTTTC 1076	Qy 961 CCTTTGGTCTCATTGCCGTTGCGATTACAGTGGTGGCGATCTTCTTGGCGGTCGACGCA 1020	QY 901 TCCTTGCCATTTTGACCGCATCAACGTTTCGCAGCAATGCGATAGATCTGAAGACTCTAA 960	Oy 841 TIAAGCCCCTACGTGAATCACAATTTGTGGGCAAAATGGCGATGTGGATGCCAGCAGGAA 900	Oy 781 TIGTTGTCGCAGTATGTGCAGTCATTACTTTTGCGCTCCGGGCGGTTCCGTTAATCC 840 Db 881 TIGTTGTCGCAGTATGTGCAGTCATTACTTTTGCGCTCCGGGCGGTTCCGTTCTTAATCC 940	Oy 721 ATCCGGTACTTCTTCTTGGGAAAGGCTGCTAAATGACAACTGATTTCTCCCTGTATTCTCC 780	Oy 661 GIGGTAATICCAGGTCAGGCCCTATITGCGGCGCTGCTGATCTTCTTGGGTCTGTGACC 720	OY 601 CGAACGAAAAAGCAGATCCCTTCTCTGCTGCTGCTGCAGGTTTGAGCTTCACCATTGCTCTT 660	Qy 541 ATTAAGGCCTCGAGTTCGCCCTTTGCTCTTTCTCACGCTGACTTTGGATTCCTGC 600	TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGAGTGGTTGATTCCTTTTGAA [44 10 1	OY 361 AACCCCATTGCCCGTTTCTATTCGGTTTTCGACGTAGGAAGCCTACGCAGTCACT 420	Qy 301 TTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA 360	Qy 241 ATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCTGGGCGCCATCGCGCTCACCACA 300	Db 281 GGCTACGAATGGTGGGCACCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAA 340	221 GCTGCAGGTTTGGGCATGTACCCGATTGGTATTTGCGTTTGGTTATTAATAC

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REFERENCE
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ATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTCTTTGTCACGCTGACTTTGGATTCCTGC
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27-OCT-1999 DE 19951708.8
NICOLE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, WALTER
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/organism="unidentified"
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Nucleotide sequence encoding the discharge of branched ami method of isolating the same and utilization thereof the patent: up 2001169788-A 26-7UN-2001;

DEGUSSA HUELS AG, FORSCHINGSZENTRUM JUELICH GMBH COCYNEBACTERIUM glutamicum ATCC13032
PN UP 2001169788-A/4
PP 2001169788-A/4
PP 24-OCT-2000 JP 2000324315
PR 27-OCT-1999 DE 19951708.8
PI NICOLE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, W
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BD014994.1 GI:225
JP 2001169788-A/4.
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    1271
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

                                                                                  Location/Qualifiers (101). (853) (853). (1176). Location/Qualifiers
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                                                                                            TCCTTGCCATTTTGACCGCATCAACGTTTCGCAGCAATGCGATAGATCTGAAGACTCTAA
                                                                                                                                             TTAAGCCCCTACGTGAATCACAATTTGTGGGGCAAAATGGCGATGTGGATGCCAGCAGGAA
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Corynebacterium glutamicum BrnE
regulator (lrp) genes, complete
AF454053
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Kennerknecht, N., Eggeling, L. a.

Direct Submission

Submitted (07-NOV-2001) IBT-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Export of L-isoleucine from Corynebacterium glutamicum: two-gene-encoded member of a new translocator family J. Bacteriol. 184 (14), 3947-3956 (2002)
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/gene="lrp"
1538. 1993
/gene="lrp"
/note="Lrp"
/codon_start=1
/transT_table=11
                                                                                                        /translation="MQKTQEIHSSLEVSPSKAALEPDDKGYRRYEIAQGLKTSLAAGL
GMYPICIAFGLLVIQYGYEMWAAPLFSGLIFAGSTEMLVIALVGAAPLGAIALTTLL
VNFRHVEYAFSFPLHVVKNPIAFFYSVFALIBEAYAVTAARPAGWSAWRLISMQIAFH
SYWVFGGLTGYKAIAELIFEISKLERPALCSLFYTLTLDSCRTKKQIPSLLAGLSFTI
ALVVIPGQALFAALLIFIGLLTIRYFFLGKAAK"
                                                                                                                                                                                                                            /note="LIV-E transporter acid export protein" /codon_start=1 /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                              /Protein_id="AAM46685.1"
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WMPAGILAILTASTERSNAIDLKTLTFGLIAVAITVVAHLLGGRRTLLSVGAGTIVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (385. .711)
/gene="brnE"
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/mol_type="genomic DNA"
/db_xref="taxon:1718"
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                                                                                                                                                                                                                                                                                                                     gene="brnF"
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SPDYFVRIGVADLEAYEQFLSSHIQTVPGIAKISSRFAMKVVKPARPQV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-MAY-2002) Satoshi Nakagawa, Kyowa Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-Tokyo 194-8533, Japan (B-mail:snakagawa@xanagen. Tel:81-44-829-3031, Fax:81-44-813-1651)
This sequence is conducted by collaboration of K Co. Ltd. And Kitasato University.
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Corynebacterium glutamicum ATCC 13032
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                              /translation="MSQNSSSLLETWRQVVADLTTLSQQADSGFDFLTPTQRAYLNLT
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PELATPORI PRETPAHNDMREWSLNPKYTFESFVIGFENFAMAANVAVAESPARAPN
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RTREEGGLITDIQFEDLETRIAILKKKAQTDGTTWDREVLELLASRFESSSIRELEGAL
IRVSAYSSLINQPIDKEMAIVALRDILPEPEDMEITAPVIMEVTAEYFEISVDTLRGA
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/note="PF00308:Bacterial dnaA protein
TIGR00362:DnaA: chromosomal replication initiator protein
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complement (1594.
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/db_xref="GI:21322765"
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/db_xref="taxon:196627"
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/gene="Cg10002"
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PF01751:Toporim domain
PF02518:Histidine kinase-, DNA gyrase B-, phytochrome-l
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VGPHRDDVDLMLGDQPAKGFASHGETWSFALSLRIAEFNLLKSDGTDFILILDDVFSE
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                                                                                                         subunit
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gene

SGC

gene

gene

SdD

Query Match Best Local Sim Matches 1076;

Similarity

100.0%; Score 1076; DB 1 ilarity 100.0%; Pred. No. 1.5e-2: Conservative 0; Mismatches

DB 1;

Length 340000; Indels

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Gaps

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gene
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complement (9471. .9914)
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                                                                                                                                                                                                                                                                                                                                                gene="Cg10010"
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Qy 121 GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC 180	QY. 61 GAACCAGATGATAAAGGTTATCGGGGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT 120	OY 1 GTGCAAAAAAGGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG 60	Query Match 70.0%; Score 753; DB 6; Length 753; Best Local Similarity 100.0%; Pred. No. 5.6e-189; Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		JOURNAL Patent: EP 1108790-A 289 20-JUN-2001; KYOWA HAKKO KOGYO CO., LTD. (JP) FEATURES Location/Qualifiers source 1753	Nakaga Yokoi, Novel	SOURCE Corynebacterium glutamicum ORGANISM Corynebacterium glutamicum Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.	VERSION AX120373 GI:14037088 KEYWORDS	AXIZO373 AXIZO3	Qy 721 ATCCGGTACTTCTTCGGAAAAGGCTGCTAAA 753 Db 721 ATCCGGTACTTCTTCTTGGGAAAGGCTGCTAAA 753		QY 601 CGAACGAAAAAGCAGATCCCTTCTCTGCTGCTGCTAGGTTTGAGCTTCACCATTGCTCTT 660	QY 541 ATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCTGC 600	OY 481 TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA 540	Qy 421 GCGGCCAGGCCCGCAGGCTGGTCGGCGTGGCGATGTCAATGCAAATAGCGTTTCAC 480	OY 361 AACCCCATTGCCCGTTTCTATTCGGTTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT 420	Qy 301 TIGCIGGIGAACTICCGCCACGIATICTAIGCGITITCAITICCGCIGCAIGIGGICAAA 360	Db 241 ATGCTGGTCATCGCCCTCGTTGTGGGGCGCCAGGGCCCCTGGGGCGCCATCGCGCTCACCACA 300

Ω. 8 60 (1	SULT 12 137710 CIUS CESSION AX137710 RSION AX137710 RSION AX137710 RSION AX137710.1 GI:14273889 TWORDS COrynebacterium glutamicum CRGANISM Corynebacterium glutamicum Bacteria; Actinobacteria;	Oy 601 CGAACGAAAAAGCAGATCCCTTCTCTGCTGCTGCAGGTTTGAGCATTGCTCTT 660	21 GCGCCAGGCCGGAGGCTGGTCGGCGTGGCGAGTTGTCTCAATGCAAATAGCGTTTCA 21 GCGCCAGGCCCGCAGGCTGGTCGGCGTGGCGAGTTGGAATAGCGTTTTCA 81 TCCTACTGGGTATTCGGCGGTCTCACCGGAGTTGGCTGTTGATTCCTTTTGA	301 TIGCTGGTGAACTICCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA 3	Db 121 GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTTTCTGTTATTCAATAC 180 181 GGCTACGAATGGTGGGCAGCCCACTGTTTTCCGGCCCTGATTTTCGCGGGCTCCACCGAA 240
Oy 661 GTGGTAATTCCAGGTCAGGCCCTATTT QY 661 GTGGTAATTCCAGGTCAGGCCCTATTT	421 dedecededecededecededeceder 481 rectaetagatatregegete	301 TTGCTGGTGAACTTCCGCC	Qy 121 GCTGCAGGTTTGGGCATGTACCCGATTG	1 GAACCAGATGATAAAGGTT	/translation="MQKTQBI GMYPIGIAFGLLVIQYGYEWW VMFRHYPYAFSEPLHVVKNPI SYWVFGGLTGVALAELIFFEI ALVVIPGQALFAALLIFLGLL ORIGIN Query Match 70.0%; Score 75

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70.0%; Score 753; DB 6; Lty 100.0%; Pred. No. 5.6e-189; ervative 0; Mismatches 0; TTCCAGGTCAGGCCCTATTTGCGGCGCGCTGATCTTCTTGGGTCTGTTGACC TTCCAGGTCAGGCCCTATTTGCGGCGCGCTGATCTTCTTGGGTCTGTTGACC AAAAGCAGATCCCTTCTCTGCTGCAGGTTTGAGCTTCACCATTGCTCTT AAAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTT GCCTCGAGTTCGCCCTTTGCTCTCTTTTGTCACGCTGACTTTTGGATTCCTGC 600 9GGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA 540 GGCCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC 480 TIGCCCGTTTCTATICGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT TGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGGCTGCATGTGGTCAAA 360 GTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC 180 GTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC 180 ATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT 120 AAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG ACTTCTTCTTGGGAAAGGCTGCTAAA 753 egetattegecegteteaceggagtegecgategeagagttgatteettttegaa GGCCCGCAGGCTGGTCGGCGACTTATCTCAATGCAAATAGCGTTTCAC 480 TIGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT reancecercerreregececaecececciregececarcececreaceae atgataaaggttatoggogotacgaaatogogoaaggtotaaaaacotocott AAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG CTTCTTCTTGGGAAAGGCTGCTAAA 753 IGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA Length 753; Indels 0; Gaps 660 540 420 420 360 720 660 600 300 720 120 60 0

bp DNA linear PAT 27-AUG-2002 the discharge of branched amino acid, and utilization thereof.

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Kennerukunehito,N., Sahm,H., Eggering,L. and Pfefferle,W.
Nucleotide sequence encoding the discharge of branched amino ac
method of isolating the same and utilization thereof
method of profise a 26-UUN-2001,
DEGUSSA HUELS AG,FORSCHUNGSZENTRUM JUELICH GMBH
OS COTYNEbacterium glutamicum ATCC14752
PN JP 2001169788-A/2
PD 26-UUN-2001
PF 24-CCT-2000 JP 2000324315
PF 27-CCT-1999 DE 19951708.8
PI NICOLE KENNERUKUNEHITO,HERMANN SAHM,LOTHAR EGGERING,WALTER PI
PFEFFERLE
PC C12N15/09,C07K14/34,C12N1/21,C12P13/06,C12P1°'
PC (C12N15/09,C12R1:15),(C12N1/21,C12P13/06,C12P1°'
PC (C12N15/00,C12R1:15)
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                                                                                TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGAICGCAGAGTTGATTCCTTTTGAA 540
                                                                                                                                           GCGGCCAGGCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC
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   ATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTCTTTGTCACGCTGACTTTGGATTCCTGC
                            ATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTCTTTGTCACGCTGACTTTGGATTCCTGC
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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100.0%; Pred. No. 5.6e-189;
tive 0; Mismatches 0;
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PATENT: UP 2002191370-A 289 09-JUL-2002;

KYOWA HAKKO KOGYO CO LITD

OS COTYNEBACTERIUM GIUTAMICUM

PN JP 2002191370-A/289

PD 09-JUL-2002

PP 15-DEC-2000 JP 2000405096

PI SATOSHI MAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI,

PI KEIKO OCHIAI,

PI KEIKO OCHIAI,

PC C12N15/09,C12N15/09,C07K14/34,C07K16/12,C07K16/40,C12M1/00, PC

C12N1/15,

PC C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12N9/02,C12P7/40,C12M1/00, PC

C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12N9/02,C12P7/40,C12P13/

PC C4,C12P13/08,

PC C4,C12P13/08,

PC C12N13/569,G01N33/68,G01N37/00//C12P21/08,(C12N1/21,C12R1:15),

PC C12N15/00,

PC C12N15/00,C12N15/00

CC C12N15/00,C12N15/00

PC C12NS/00,C12N15/00

PC C12NS/00,C12NS/00

PC C12NS/00

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Yokoi,H., Tateishi,N., Sem
Novel polymucleotide
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GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC 180
                                                         GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAACCTCCCTT
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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	4 from patent US 6613545. 1 GI:40115726 Lied. 1 to 324) 1 to 324) 1 echt,N., Sahm,H., Eggeling,L. and Pfefferle,W. 1 de sequences coding for the export of branched chain ami 1 rocess for the isolation thereof and use thereof 1 US 6613545-A 4 02-SEP-2003; 1 Location/Qualifiers 1 .324 /organism="unknown" /mol_type="genomic DNA" 10 .30.1%; Score 324; DB 6; Length 324; 10 .30.1%; Pred. No. 5.5e-75; 11	CIGATITICGCGGGCTCCACCGAA 2 CIGGGGCCATTCGCGGGCTCCACCAA 3 CITGGGCGCCATCGCGCTCACCACA 3 CITGGGCGCCATCGCGCTCACCACA 3 CITGATTCCCGCTGCATTGGTCACACA 3 CITGATTCCCGCTGCATTGGTCACACA 3 CITCATTCCCGCTGCATTGGTCACCACA 3 ATCCACGAAGAGCCTACGCAGTCACT 4 ATCCACAAGAGCCTACGCAGTCACC 4 ATCCTCAATGCAAATAGCGTTTCAC 4 ATCCTCAATGCAAATAGCGTTTTCAC 4 ATCCTCAATGCAAATAGCGTTTTCAC 4 ATCCTCAATGCAAATAGCGTTTTCAC 4 ATCCTCAATGCAAATAGCGTTTTCAC 4 ATCCTCAATGCAAATAGCGTTTTCAC 6 ATCGCAGAGTTGATTCCTTTTGAA 5 ATCGCAGAGTTGATTCCTTTTGAA 5 ATCGCAGAGTTGATTCCTTCTGC 6 CTGATCTTCACCTTTGGATTCCTGC 6 GGTTTGAGCTTCACCATTGCTCTT 6 GGTTTGAGCTTCACCATTGCTCTT 6 GGTTTGAGCTTCACCATTGCTCTT 6 CTGATCTTCTTGGGTCTGTTGACC 7 CTGATCTTCTTGGGTCTGTTTGACC 7 CTGATCTTCTTGGGTCTGTTTGACC 7 CTGATCTTCTTTGGGTCTTTTGACC 7 CTGATCTTCTTTGGGTCTTTTGACC 7 CTGATCTTCTTTGGGTCTTTTGACC 7 CTGATCTTCTTGGGTCTTTTGACC 7 CTGATCTTCTTTGGGTCTTTTGACC 7 CTGATCTTCTTTGGGTCTTTTTTTTTTTTTTTTTTTTTT

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ALIGNMENTS

AAH21109 standard; DNA; 1271

ΒP

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L-amino acid production; brnF; brnE; branched-chain amino acid; coryneform bacterium; leucine; isoleucine; valine; medicine; animal nutrition; ds.
                                                                                                                                                                                                                                                                                                                                  C. glutamicum DNA encoding brnF and brnE
                                                            WPI; 2001-391595/42.
P-PSDB; AAB86247, AAB86248.
                                                                                                                                                                                                                                                                                                                                                    05-SEP-2001 (first entry)
                                 New export genes from coryneform bacteria, useful for increasing fermentative production of branched-chain amino acids.
                                                                                                                                   27-OCT-1999; 99DE-01051708.
                                                                                                                                                    11-OCT-2000; 2000EP-00122057
                                                                                                                                                                      02-MAY-2001.
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                                                                                                                                                                                                                                                                              Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                      AAH21109;
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                                                                                                         (DEGS )
                                                                                                         DEGUSSA AG. FORSCHUNGSZENTRUM JUBLICH GMBH.
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/product= "brnF"
853. .1179
                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                         'product= "brnE"
                                                                                       Sahm H, Pfefferle
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Ω

This invention describes a novel isolated polynucleotide

(I) containing

Claim 4 (i); Page 13; 23pp; German

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CC at least one sequence that (1) is 70% identical with a sequence that CC encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) (2) cip (3) encodes a polypeptide at least 70% identical with (3) (2) cr (5); (iii) is the complement of (1) or (ii), or (10) contains at least CC 15 consecutive bases from (1)-(iii). The invention also describes (a) (2) coryneform microorganisms, especially Corynebacterium, transformed with CC coryneform microorganisms, especially Corynebacterium, transformed with CC one or more (1), where these are replicative DNA; (c) production of CC branched-chain 1-aa by fermentation of coryneform bacteria in which the CC branched-chain 1-aa by fermentation of coryneform bacteria in which the CC branched-chain production of production of coryneform bacteria being CC especially overexpressed; and (d) method for isolating the brnE and/or CC brnF genes. (I) is used for transformation of coryneform bacteria being CC used for fermentative production of branched-chain amino acids, specifically leucine, isoleucine and valine, which are useful in medicine and animal nutrition. (I) can also be used as source of primers and CC probes for isolation of related sequences. Transformation with (I) CC corynebacterium glutamicum ATCC 14752 brnF and brnE proteins described in the method of the invention
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Best Local Similarity
Matches 1076; Conserv
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GTGGTAATTCCAGGTCAGGCCCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACC
                                                                                                        CGAACGAAAAAGCAGATCCCTTCTCTCCTCCTCGCAGGTTTGAGCTTTCACCATTGCTCTT
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                                                                           CGAACGAAAAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTT
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RESULT 2
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XX AAH22
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AX AAH22
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XX COTY
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This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that encodes at least one of 251 amino acid (aa) (3) or 108 aa (5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-amino acid production; brnF; coryneform bacterium; leucine; animal nutrition; ds.
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                                                                                            (i); Page 17-18; 23pp;
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CC polypeptides; (ii) encodes a polypeptide at least 70% identical with (3) CC or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least CE 15 consecutive bases from (i)-(iii). The invention also describes (a) CC corpneform microorganisms, especially Corynebacterium, transformed with CC one or more (I), where these are replicative DNA; (c) production of CC branched-chain L-aa by fermentation of coryneform bacteria in which the CC brill and/or bril genes (or equivalent sequences) are amplified, CC especially coverexpressed; and (d) method for isolating the bril and/or CC bril genes. (I) is used for transformation of coryneform bacteria being CC used for fermentative production of branched-chain mino acids, cc specifically leucine, isoleucine and valine, which are useful in medicine and animal nutrition. (I) can also be used as source of primers and corynebacterium glutamicum ATCC 13032 bril and bril proteins described in CC corynebacterium glutamicum ATCC 13032 bril and bril proteins described in CC the method of the invention
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26-SEP-2001 AAH64966 standard; (first DNA; entry) 349980 ₽P

Coryneform bacterium; amino organic acid synthesis; ds. organic glutamicum coding sequence fragment SEQ ID acid synthesis; vitamin; saccharide;

NO:

Corynebacterium glutamicum

20-JUN-2001

18-DEC-2000; 2000EP-00127688

16-DEC-1999; 99JP-00377484. 07-APR-2000; 2000JP-00159162. 03-AUG-2000; 2000JP-00280988.

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(KYOW) KYOWA HAKKO KOGYO Ŗ

'nά Mizoguchi Senoh A, i H, Ando Ikeda M, S, Hayashi Ozaki A; 3 Ochiai Ķ Yokoi

Ξ

WPI; 2001-376931/40.

Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.

Claim 7; SEQ ID NO 1; 246pp + Sequence Listing; English.

RESULT 3
AAH64966
AN
AAH64966
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AAH64
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AAH64
AN
AAH66
AN
AAH66 The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained

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ATCCGGTACTTCTTCGGGAAAGGCTGCTAAATGACAACTGATTTCTCCTGTATTCTCC

_	CGCA 1020	 CCTTTGGTCTCATTGCCGTTGCGATTACAGTGGTGGCGCATCTTCTTGGCGGTCGACG 	96	γ _ν ογ
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	그급	CCTTGCCATTTTGACCGCATCAACGTTTCGCAGCAATGCGATAGATCTGAAGACT	96	γ
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	TCTT 660 TCTT 277488	1 CGAACGAAAAAGCAGATCCCTTCTCTGCTGCTGCTGCAGGTTTGAGCTTCACCATTGCTCTT	60 27742	р Q
	CTGC 277428	9 ATTAAGGGCCTCGAGTTCGCCCTTTGCTCTTTGTCACGCTGACTTTGGATTCCTGC	27736	Дb
	CTGC 600	41 ATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTCTTTGTCACGCTGACTTTGGATTC	5 4	Ş
	TGAA 277368	9 TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGAGAGTTGATTCCTTTTGAA	27730	Дb
	TGAA 540	1 - T.C	48	Ş
	 CAC 277308	9 GCGGCCAGGCCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC	27724	망
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	N)	9 TIGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA	27712	당
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	ips 0;	თს	atches 107	Ma
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Query Match 70.0%; Score 753; DB 4; Length 753; Best Local Similarity 100.0%; Pred. No. 8.1e-227; Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps

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bring genes. (I) is used for transformation of coryneform bacteria being bring genes. (I) is used for transformation of coryneform bacteria being used for fermentative production of branched-chain amino acids, specifically leucine, isoleucine and valine, which are useful in medicine and animal mutrition. (I) can also be used as source of primers and probes for isolation of related sequences. Transformation with (I) increases yield of branched-chain amino acids. This sequence encodes the corynebacterium glutamicum ATCC 14752 brnF protein described in the method of the invention Sequence 753 BP; 140 A; 211 C; 194 G; 208 T; 0 U; 0 Other;	s invention describes a novel isolated polynucleotide (I) con least one sequence that (i) is 70% identical with a sequence pleast one of 251 amino acid (aa) (3) or 108 aa (5) yepptides; (ii) encodes a polypeptide at least 70% identical (5); (iii) is the complement of (i) or (ii), or (iv) contain consecutive bases from (i) (iii). The invention also describete the form sequences of 753 bp (2) or 324 bp (4); (b) yepform microorganisms, especially Corynebacterium, transform or (ii), where these are replicative DNA; (c) production or more (I), where these are replicative DNA; (c) production ched-chain L-aa by fermentation of coryneform bacteria in when the sequences of the production of the form of the production of the form sequences of the production of the form of the production of the productio	P-PSDB; AAB86247. New export genes from coryneform bacteria, useful for increasing fermentative production of branched-chain amino acids. Claim 5; Page 14-15; 23pp; German.	(DEGS) DEGUSSA AG. (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH. Kennerknecht N, Eggeling L, Sahm H, Pfefferle W;	02-MAY-2001. 11-OCT-2000; 2000EP-00122057. 27-OCT-1999; 99DE-01051708.	nal nutrition; ds. nal nutrition; ds. nebacterium glutamicum. 196010-Al.	21110; SEP-2001 (first entry) Slutamicum brnF DNA. nino acid production; brnF; brnE; branched-cha	UULT 4 121110 AAH221110 standard; DNA; 753 BP.	1021 CCTTGTTGAGCGTTGGCGCTGGCACCATCGTTTTTGTTGGACTGGTGAATCTTTTC 1076	

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Sequence 753

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07-APR-2000;
03-AUG-2000;
                                                                The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium. And identifying a homologue of a gene derived mor coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
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Ś 맑 ঠ 밁 S 밁 S 밁 ঠ 片 5 뮍 S 밁 Ś 밁 Ş Query Match Best Local S Matches 753 Local Similarity 421 361 361 301 301 181 121 481 421 241 241 181 121 61 6 753; GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAA GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTTGGTCTCTTGGTTATTCAATAC GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT GTGCAAAAAACGCAAGAGTTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA AACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT TTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA ATGCTGGTCATCGCCCTCGTTGTGGGCCGCAGCGCCCTGGGCCCCATCGCGCTCACCACA ATGCTGGTCATCGCCCTCGTTGTGGGCGCCAGCGCCCCTGGGCGCCCATCGCGCTCACCACA GGCTACGAATGGTGGGCAGCCCACTGTTTTCCGGGCCTGATTTTCGCGGGCTCCACCGAA GCGGCCAGGCCCGCAGGCTGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC 70.0%; Score 753; DB 5; Lilarity 100.0%; Pred. No. 8.1e-227; Conservative 0; Mismatches 0; Length 753; Indels 0 Gaps 540 420 360 360 300 180 120 480 480 420 300 240 240 180 120 60

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                                                                                                                                                                 This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to corynebacterium glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
                                                                                                                                                                                                                                                                                                New nucleic acid array useful for Corynebacterium glutamicum during from Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum
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                                                Claim 5; Page 16; 23pp;
                                                                                            New export genes from coryneform bacteria, useful for fermentative production of branched-chain amino acids
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                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                      Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
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04-JUN-2003

(first entry

ACA01970 standard; DNA; 324

ВP

1052 240 992 180 932 120 872 60

C. glutamicum derived ORF SEQ ID 1961.

nucleic acid array;

fermentation; culture;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 324 BP; 60 A; 79 C; 80 G; 105 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
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Tateishi N,
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03-AUG-2000; 2000JP-00280988.
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                                                                                                                                                                                                                                                                                     GCGCTCCGGGCGGTTCCGTTAATCCTTAAGCCCCCTACGTGAATCACAATTTGTGGGC
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                        TTTGTTGGACTGGTGAATCTTTTC 1076
                                                                       GTGGCGCATCTTGTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTT
                                                                                          GTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTT
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Senoh A,
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Ikeda M,
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Pred. No. 1.5e-91;
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Ozaki A;
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RESULT 10
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AC AAF616
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Best Local S
Matches 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to corynebacterium glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Farwick M, Moeckel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 324 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid array useful for Corynebacterium glutamicum during from Corynebacterium glutamicum.
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             C. glutamicum
                                         12-JUL-2001
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                                                                                                                                                                                                                                                                                 AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGGATTACAGTG
                                                                                                                                                                                                                                                                                                                                          AAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTTCGC
                                                                                           standard;
                                                                                                                                                                          TTTGTTGGACTGGTGAATCTTTTC 1076
                                                                                                                                                                                                                                      GTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTT
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 324;
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RESULT 11
AAF61695/c
ID AAF616
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AC AAF616
XX
AC AAF616
XX
DT 12-JUL
XX
DE C. glu

AAF61695

standard; DNA; 778

C. glutamicum

lrp

encoding

DNA

fragment

SEQ

ij

12-JUL-2001 AAF61695;

(first entry)

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Query Match
Best Local S
Matches 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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276;
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                                                                                                                                                                                                                                                               224 GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAACCTCCCTT
                                                                                                                                                                                                                                                                                                                                                   284 GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG
44
                                                                                                                                                                                                                                                                                                       61 GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT
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                                                                                                                                                                                                                                                                                                                                                                                   GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCTG
                           ATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCCTGG 280
                                                                                                               GGCTACGAATGGTGGGCAGCCCCACTGTTTTTCCGGGCCTGATTTTTCGCGGGGCTCCACCGAA
                                                                                     GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGGCTCCACCGAA
                                                                                                                                                                           GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC
ATGCTGGTCATCGCCCTCGTTGTGGGCGCACGCCCCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 16; 22pp; German.
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particularly lysine and isoleucine.
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Matches 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     animal feed supplement. It may also be used as probes and particularly as isolating related sequences. Regulating expression of [1] improves production of amino acids, especially of L-lysine. This sequence encodes a fragment of the Corynebacterium glutamicum lrp protein which is used in the method described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coryneform bacteria used for the fermentative production of selected L amino acids, by fermenting the amino acid-producing coryneform in which at least the lry gene has been weakened or amplified, then isolating amino acids that have accumulated in the medium or cells. (I) is used transform coryneforms for production of L-amino acids, specifically lysine and isoleucine, which are used in medicine and particularly as animal feed sunniament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel isolated nucleic acid (I) coryneform bacteria used for the fermentative production o
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                26-SEP-2001
                                          AAH68373
                                                                   AAH68373 standard;
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supplement; ds.
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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Tateishi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynuclectides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
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)B; AAG93154.
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                                                CGGCCAGGCCCGCAGGCTGGTCGGCGTG---GCGACTTATCTCAATGCAAATAGCGTTTC
                                                                                                      CCGGCGCCGGCCCCTATTCCACCTACGCGCTTACCGACGAGTCCTACGCCATCGTGT
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Senoh A,
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2000JP-00280988.
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Ikeda M,
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Ozaki A;
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2.7e-29;
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                                                                                                                This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to corynebacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
                                                                              Sequence 711 BP; 123
                                                                                                                                                                                                                                      Claim 1; Page 456; 709pp; German.
                                                                                                                                                                                                                                                              New nucleic acid array useful for Corynebacterium glutamicum during from Corynebacterium glutamicum.
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                                                                                                                                                                                                                                                                                                                                             Farwick M, Moeckel B,
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Pred. No. 2.7e-
0; Mismatches
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RESULT 14
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  Nakagawa S,
Tateishi N,
                                                                                                                      16-DEC-1999; 99JP-00377484.
07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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Senoh A, Ikeda M,
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S, Hayashi M,
Ozaki A;
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Matches 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
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larity 51.5%; Pred. No. 6e-
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C. glutamicum derived ORF SEQ ID 1959.
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                                                                                                                                                                 1 GTGCAAAAAACGCAAGAGATTCATTCAAGCCCTGGAGGTGTCGCCCATCCAAGGCAGCCCTG
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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RESULT 2
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Sequence 6, Application US/09471803A
PATERIX NO. 6613545
GENERAL INFORMATION:
APPLICANT: KENNERKNECHT, NICOLE
APPLICANT: SAHM, HERMANN
APPLICANT: EGGELING, LOTHAR
APPLICANT: PREFERLE, WALTER
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: ASOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/265496/MAS
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FEATURE:
NAME/KEY: gene
LOCATION: (101)..(853)
OTHER INFORMATION: brnF
NAME/KEY: gene
LOCATION: (853)..(1176)
OTHER INFORMATION: brnE
OTHER INFORMATION: ATCC13032
US-09-471-803A-6
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CURRENT FILING DATE: 1999-12-23;
PRIOR APPLICATION NUMBER: DE 199 51 708.8;
PRIOR FILING DATE: 1999-10-27;
NUMBER OF SEQ ID NOS: 12;
SOFTWARE: PATENTIN Ver. 2.1;
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LENGTH: 1271
TYPE: DNA
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GENERAL INFORMATION:

APPLICANT: KENNERKNECHT, NICOLE

APPLICANT: SAHM, HERMANN

APPLICANT: SAEM, HERMANN

APPLICANT: BEGGELLING, LOTHAR

APPLICANT: PFEFFERLE, WALTER

TITLE OF INVENTION: NUCLECTIDE SEQUENCE CODING FOR THE EXPORT OF

TITLE OF INVENTION: BRANCHED CHAIN ANINO ACIDS, PROCESS FOR THE

TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF

FILE REFERENCE: 21123/265496/MAS

CURRENT APPLICATION NUMBER: US/09/471,803A

CURRENT FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: DE 199 51 708.8

PRIOR APPLICATION NUMBER: DE 199 51 708.8

PRIOR FILING DATE: 1999-10-27

NUMBER OF SEQ ID NOS: 12

SOPTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 753

TYPE: DNA

ORGANISM: Corynebacterium glutamicum

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                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(753)
OTHER INFORMATION: brnF
OTHER INFORMATION: ATCC14752
                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                     GGCTACGAATGGTGGGCAGCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAA 240
                                                                              GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTTGGTCTCTTGGTTATTCAATAC
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APPLICANT: KENNERKNECHT, NICOLE
APPLICANT: SAHM, HERWANN
APPLICANT: SAHM, HERWANN
APPLICANT: SEGELING, LOTHAR
APPLICANT: PEFFERLE, WALTER
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: REACHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/265496/MAS
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID MOS: 12
SOFTMARE: PATENTIN VET: 2.1
SEQ ID NO 4
LENGTH: 324
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                                                                     ; NAME/KEY: CDS
; LOCATION: (1)..(324)
; OTHER INFORMATION: brnE
; OTHER INFORMATION: ATCC14752
US-09-471-803A-4
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US-09-471-803A-4
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     Matches
                    Query Match
Best Local
                                                                                                                                                            TYPE: DNA ORGANISM: Corynebacterium glutamicum FEATURE:
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     Conservative
                    30.1%;
Score 324; DB 4; L
s; Pred. No. 8.1e-96;
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RESULT 5
US-09-489-039A-3016
US-09-489-039A-3016
; Sequence 3016, Application US/09489039A
; Patent No. 6610836
; Patent No. 6610836
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US-08-232-463-14
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3016
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 3016
LENGTH: 756
TYPE- NY 56
 Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 130; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA-
TITLE OF INVENTION: PNEMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
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                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                 95 TCGCGCAAGGTCTAAAAACCTCCCTTGCTGCAGGTTTGGGCATGTACCCGATTGGTATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAATGGCGATGTGGATGCCAGCAGGAGCTTTTGCCATTTTGACCGCATCAACGTTTTGGC
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                                                                                                                                                                                 CCCTGGGCGCCATCGCGCACCATTGCTGGTGAACTTCCGCCACGTATTCTATGCGT 334
                                                                                                                                                                                                                GCATTATTTACGCCGGCGCCAGCCAGTTTGTGATCACCGCCATGTTGGCCGCCGGCAGTT
                                                                                                                                                                                                                                      GCCTGATTTTCGCGGGGCTCCACGAAATGCTGGTCATCGCCCTCGTTGTGGGGCGCAGCGC
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                                                                                          CTTCACTGC 310
                                                                                                                         TTTCATTCC 343
                                                                                                                                                      CGCTGTGGGTCGCCGCCCTGACGGTGATGGCGATGGATGTCCGCCACGTGCTGTATGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                              52.2%;
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; CLONE: pTZgpt-1
US-08-232-463-14
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APPLICANT: DORNER
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ZIP: 22313-0299
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                                                                                                                                          1230
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Query Match 4.9%; Score 52.4; DB 1; Best Local Similarity 3.6%; Pred. No. 3e-06; Matches 14; Conservative 221; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEC ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM For Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F.G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1800 Dia
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                   460 TCAATGCAAATAGCGTTTCACTCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                     ATCTTCTTGGGTCTGTTGACCATCCGGTACTTCTTCTTGGGAAAGGCTGCTAAAIGACAA 759
                                                                                                                                                                                                                                                                                         CTGATTTCTCCTGTATTCTCCTTGTTGTCGCAGTATGTGCAGTCATTACTTTTGCGCTCC
                                                                                                                                              ACGCTGACTTTGGATTCCTGCCGAACGAAAAAGCAGATCCCTTCTCTGCTGCTCGCAGGT
TTGAGCTTCACCATTGCTCTTGTGGTAATTCCAGGTCAGGCCCTATTTGCGGCGCTGCTG
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1800 Diagonal Road,
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1266:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-Jun-1998

PRIOR APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1410 YYYYYYYYYYYYYYYYYYYYTTACCAA 1441
                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature LOCATION: (B) LOCATION 1...768 SEQUENCE DESCRIPTION: SEQ ID NO: 1266:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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  212
                                    227
                                                                             152 TTGGGAAAGCTGCCGGATTTCATCCACTAGTCGTCACGTTGATGTCCCTGCTGGTCTATG
                                                                                                                                                                                               107 TAAAAACCTCCCTTGCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTTGGTCTCT 166
                                                                                                                    167 IGGITATICAATACGGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCG
                                                                                                                                                                                                                                          al Similarity 49.:
104; Conservative
                                                                                                                                                             92 TCANAGACACGTTACCTACCGTTTTCGGTTATATCGGTATTGGACTTGCATTTGGTATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
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                                      ceeecrocacceaaarecreercarceccrocrocrocaceececaececccreeecececa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 768 base pairs
  TCTGCCCAATTTATCACAGTCAGCATGCTTGCTAGTCACAGCCCATTGCTTTCCA
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209 TTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCG 268

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Query Match
Best Local Similarity
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11376
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                                                                           ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: AUGUSTO FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107195.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11376, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                    SEQ ID NO 11418
LENGTH: 1086
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11418, Application US/09252991A
Patent No. 6551795
Matches
                  Query Match
Best Local :
                                                                                                                                                                      APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AUGUSIOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-07-18
PRIOR PILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
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                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 TCGCGCTCACCACATTGCTGGTGAACTTCCG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 GIGCCGGGTTCTTTTCGATCATCTTCACCACCTCCTCCTGACCTCGCAGCACCTGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 CAGCGCCCTGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTTCCGCCACGTATTCT
Similarity 77; Conserv
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Conservative
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                55.0%;
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                  Score 39.2; DB Pred. No. 0.019;
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                                     DB 4;
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                                     Length 1086;
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RESULT 10
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US-09-621-976-8976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT PAPLICATION UNBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 8976
LENGTH: 399
                                                                                                              NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 18033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards,
APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                       Sequence 18033,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    Patent No. 663906
                                                                                                                                                                                                                                                                                                                                                                            -09-621-976-18033
                                                                                                                                                                       APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Giordano, J.Y. TITLE OF INVENTION: ESTS and FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dumas Milne Edwards, APPLICANT: Jobert, S.
                                                TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc_feature
LOCATION: 16
                                                                                           LENGTH: 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       509 GAGTGGCGATCGCAGAGTTGATTCCTTTTGAAATTAAGGGCCTCGAGTTCGCCCTTTGCT 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTCCGCCATCGTCTTCGCCGGCGCCCCAGTTGGTGGCGATCGGCATGCTCAAGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYRGSTYKCWKAYYTKKRRKWTRWTYYYYKSYNSMKKTWRMKTAYYWTKRWKMTRTKWTW 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIGCCGGGTTCTTTCGATCATCTTCACCACCCTCCTCGTGACCTCGCAGCACCTGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGCGCCCTGGGCGCATCGCGCTCACCACATTGCTGGTGAACTTCCGCCACGTATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMKWGKSMWWKWTYYYYYYMMKWSKMTYWSMMSCYARKCWRTYAKTYTWMTCMTWGKRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGCGCTGCTGATCTTGGGGTCTGTTGACCATCCGGTACTTCTTCTTGGGAAAGGCT 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIMCWXCTTYWMAGIMMYRYRRYWYYAKRAKWSKRCIWSTICYCMKYMAKKCWSYWWSMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCTCGCAGGTTTGAGCTTCACCATTGCTCTTGTGGTAATTCCAGGTCAGGCCCTATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAMWRKKKWICWKGRSSWGSRSIGYYAWMYKKSWCISRKWMYYKKRRKKWRRKCISIKRI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGGCATGAGCTTGCGGCCG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCGTTTTCATTCCCGCTG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                         Application US/09621976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.6%;
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Pred. No. 0.012;
.2; Mismatches
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                                                                              RESULT 13
US-09-252-991A-2761
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US-09-252-991A-3205/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3205
LENGTH: 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3205, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
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                   Patent No. 6551795
GENERAL INFORMATION:
                                          Sequence 2761, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
mes 49; Conserv
                                                                                                                                                                                                                                                                                                          3.4%;
Local Similarity 58.0%;
es 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
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                                                                                                                                                            405
                                                                                                                                                                                                  271
                                                                                                                                                                                                                                           465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 MCCYYMRKTTYCMMWYSRWWRGSMWTARGAWWMCYWWYY 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  662 TGGTAATTCCAGGTCAGGCCCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 WKRWYCSSCCMMYTKGGGSMWTTTWMMRRRKKSYKRWTKGKKKKKTTWMMAAMCYTTWRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           482 CCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACGAAAAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMYKGGRMYWWWRGGMWKRMYWMYKKKSMWKGSCMWKRAWWARKTTYYTWAWYYTTYYKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSGNCYYCCMARKWRSYKGGRMYKSMRGSSSCYKSCMMCKMSKYCSGSYKKTTTTTTWAW
                                                                                                                                                                                                  GCGCCCCTGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTTCCGCCACG 322
                                                                                                                                                                                                                                        TACTICCIGATCAACCICGGCGCCGCCCCCCGCTGATCGGCCTGACTCTCGGCGTC 406
                                                                                                                                                                                                                                                                             rcceecciearmiceceeecrecaeceaaaarecieercareeccicerieieeececa 270
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                                                                                                                                                            GCCGCCCAGGCCGCACCTTCCTGGTCACCGCGCTGGTCTACTTCTGCTACG
  Marc J.
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    Rubenfield et al
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14.4%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                        Score 36.8; DB Pred. No. 0.12;
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                                                                                                                                                                                                                                                                                                                                                             Length 1140;
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Matches

TYPE: DNA

RESULT

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62

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; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-09-020-956-12/c
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Best Local Similarity 58.0
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/09020956
Patent No. 6261562
Query Match
3.4%;
Best Local Similarity 59.8%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-252-991A-2761
                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARS: PatentIn Release #1.0, V
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/09/020,956
APPLICATION NUMBER: US/09/020,956
                                                                                                                                                                                                                                                                                                 FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY, AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2061
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                     TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Xu, Jiangchun APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 550.
                                                                                                                                                  LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 TCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCGCA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGCCCTGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTTTCCGCCACG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGCCCAGGCCACCTTCCTGGTCACCGCGCTGGTCTACTTCTGCTACG 1384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                  linear
                                                                                                                                                                                                                                                                                   (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.4%; Score 36.8; DB 4; Length 2061; 58.0%; Pred. No. 0.17; 1tive 0; Mismatches 47; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Release #1.0, Version #1.30
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  Score 36.4; DB 3; Length 751; Pred. No. 0.12; 0; Mismatches 39; Indels
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Search completed: April 19, 2004, 18:38:09 Job time : 96.5988 весв

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2IP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/030,607

FILING DATE: 25-FEB-1998

CLASSIFICATION: NOTAMATION:

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.427C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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US-09-030-607-12
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, COMPOUNDS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd

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Minimum
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Maximum Match 100%
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US-10-767-701-7545
US-10-767-701-744
US-10-767-701-744
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Sequence 1266, Ap
Sequence 5263, Ap
Sequence 10866, A
Sequence 983, App
Sequence 11511, Ap
Sequence 7545, Ap
Sequence 744, App
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         62, Appl
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RESULT 2
US-10-417-884A-1266
JS-10-417-884A-1266
Sequence 1266, Application US/10417884A
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
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.0 1306 6 US0 1465 7 US-6 .0 1465 7 US-6 .0 1532 7 US-6 .0 1532 7 US-6 .0 1625 7 US-6 .0 1625 7 US-6 .0 1625 7 US-7 .0 1625 7 US-7 .0 321019 6 US-7 .0 321019 7 US-7 .0 321019 7 US-7 .0 321019 6 US-7 .0 321019 7 US-7 .0 321019 6 US-7 .0 321019 7 US-7 .0 321019 7 US-7 .0 321019 7 US-7 .0 321019 6 US-7 .0 321019 7 US-7 .0 32101	.0 1306 6 US-10-775-920-134 Sequence .0 1465 7 US-60-552-390-623 Sequence .0 1465 7 US-60-552-390-627 Sequence .0 1465 7 US-60-552-390-627 Sequence .0 1532 7 US-60-552-390-627 Sequence .0 1532 7 US-60-552-390-625 Sequence .0 1625 7 US-60-552-390-625 Sequence .0 228854 7 US-60-548-091-5604 Sequence .0 321019 6 US-10-96-307-259 Sequence .0 321019 6 US-10-796-307-879 Sequence .0 321019 6 US-10-796-307-879 Sequence .0 321019 6 US-10-796-307-8770 Sequence .0 32644 6 US-10-796-307-8770 Sequence .0 112486 6 US-10-767-701-3886 Sequence .9 5448 1 PCT-US03-38865-2	31.6	31.6	31.8	32	32	32	32	32.2	32.2	32.2	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	24.10
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	6 US-10-775-920-134 6 US-10-775-920-134 7 US-60-552-390-623 7 US-60-555-303-461 7 US-60-555-303-461 7 US-60-555-303-467 7 US-60-555-303-467 7 US-60-555-303-460 7 US-60-555-303-460 7 US-60-555-303-460 7 US-60-555-303-460 1 PCT-US04-07467-29 7 US-60-548-091-5604 8 Equence 1 US-10-848-091-5604 8 US-10-796-307-259 8 Equence 6 US-10-796-307-8770 8 Equence 6 US-10-796-307-8770 8 Equence 6 US-10-796-307-8770 9 Sequence	2.9	2.9	3.0	3.0	3.0	3.0	3.0	3.0									3.0	ω. 0	
	6 US-10-775-920-134 6 US-60-552-390-623 7 US-60-552-390-623 8 Equence 7 US-60-555-303-461 8 Equence 7 US-60-555-303-467 8 US-60-555-303-627 8 US-60-555-306-25 9 US-60-555-306-25 9 US-60-555-306-25 9 US-60-552-390-625 9 US-60-552-390-625 9 US-60-552-390-625 9 US-60-552-390-625 9 US-60-552-390-625 9 US-60-548-091-5634 9 US-10-848-091-5634 9 US-10-796-307-259 9 US-60-548-091-764 9 US-10-796-307-8771 9 US-60-548-091-765 9 US-10-796-307-8771 9 US-60-548-091-767-8770 9 US-60-796-307-8770 9 US-60-767-471-10642 9 US-10-767-471-10642	5448	715	112486	84156	32644	1271	1202	321019	321019	228854	2772	1625	1625	1532	1532	1465	1465	1306	
US-10-775-920-134 US-60-552-390-623 US-60-552-390-627 US-60-555-303-451 US-60-555-303-457 US-60-555-303-450 PCT-US04-07467-29 US-60-548-091-5503 US-10-803-180-1664 US-10-796-307-259 US-10-796-307-259 US-10-796-307-259 US-10-796-307-259 US-10-796-307-259 US-10-796-307-259 US-10-796-307-259 US-10-796-307-259 US-10-796-307-8771 US-10-796-307-8770	sequence	<u>, , , , , , , , , , , , , , , , , , , </u>		on.	o	o	0			თ	7		7		7	7	٦,	7	ው	•
		PCT-US03-38685-2	US-10-767-701-3886	US-10-767-471-10642	US-10-796-307-8770	US-10-796-307-8771	US-10-796-307-259	US-10-796-307-258	US-60-548-091-5604	US-10-803-180-1664	US-60-548-091-5633	PCT-US04-07467-29	US-60-555-303-460	US-60-552-390-625	US-60-555-303-457	US-60-552-390-627	US-60-555-303-461	US-60-552-390-623	US-10-775-920-134	

ALIGNMENTS

Sequence 10854, Application US/10767701 GENERAL INFORMATION: APPLICANT: Kovalic, David K. APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules a TITLE OF INVENTION: Plants and Uses Thereof FILE REFERENCE: 38-21(53535)B CUTRENT APPLICATION NUMBER: US/10/767,701 CUTRENT APPLICATION NUMBER: US/10/767,701 CUTRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128 SEQ ID NO 10854 LENGTH: 1014 TYPE: DNA CRGANISM: Sorghum bicolor FEATURE: COURSE THEOREMATTON: Close ID: CORPAT-78MAY01-; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS47627_1 US-10-767-701-10854 US-10-767-701-10854 RESULT 1 Matches Query Match Best Local 131 142 191 GGTGGGCAGCCCAACTGTTTTCCGGCCTGATTTTCGCGGGGCTCCAACCGAAAATGCTGGTCA 202 105; 80 22 Similarity AGTCCTGGGGCCCTCTCTTTGGCAAGGTGTTCTTCGCCGCCTCGGTCGTCGCCCACCTCG gécégérécrésisés de la recressión de la regecareraccearregrarrecerrregrererrerrearracearraceaar GGTCCGTCCTCGCCTCCGTCTTCTCCCCTCC 234 ACTICCGCCACGTATICTATGCGTTTTCATICC 343 TCGCCCTCGTTGTGGGCGCAGCGCAGCCGCTGGGCGCACATCGCGCGCTGACATTGCTGATA 310 redrecreancaredresecures reserves cricices eccesecreates en reserves establishes executados en reserves establishes establishes en reserves establishes establishes en reserves establishes establishe Conservative 49.3%; Acid Molecules and Ot and Uses Thereof For 0; Score 40.2; DB 6; Length 1014; Pred. No. 0.0073; Oj. Mismatches 108; Indels 0 Other Molecules Associated With or Plant Improvement 0 Gaps 201 141 250 81 0

and David Bush AND AMINO ACID SEQUENCES RELATING TO FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION

100 Beaver Street

NUMBER OF SEQUENCES:

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NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...768
LOCATION: SEQUENCE DESCRIPTION: SEQ ID NO: 1266:
US-10-417-884A-1266
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US-10-767-701-5263
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NAME: ATINIALLO, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPHAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1266:
SEQUENCE CHARACTERISTICS:
Sequence 5263, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 3.7%;
Local Similarity 49.3%;
les 104; Conservative
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MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/417,884A FILING DATE: 17-Apr-2003 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                      272
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FILING DATE: 30-Unn-1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                    TCAAAGACACGTTACCTACCGTTTTCGGTTATATCGGTATTGGACTTGCATTTGGTATCG
                                                                                                                                                                                                                                                                                                                                                                                                         TAAAAACCTCCCTTGCTGCAGGTTTGGGCATGTACCCCGATTGGTATTGCGTTTTGGTCTCT 166
                                                                                                                                        TCGTTTTCTCGACCTTTCTAGTCAATTCCCG 302
                                                                                                                                                                                                                                                    CGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCCTGGGGCGCCA 286
                                                                                                                                                                                                                                                                                           TTGGGAAAGCTGCCGGATTTCATCCACTAGTCGTCACGTTGATGTCCCTGCTGGTCTATG
                                                                                                                                                                                                                                                                                                                              TEGITATICAATACGGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGGCCTGATTTTCG 226
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Pred. No. 0.0085;
0; Mismatches 107;
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RESULT 5 US-10-100-683-983/c

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US-10-767-701-10866
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 5263
SEQ ID NO 5263
SEQ ID NOS: 63128
SEQ ID NOS: 63128
OF GANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS111974_1
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US-10-767-701-10866
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Best Local S
Matches 88
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CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 10866
LENGTH: 1034
TYPE: DNA
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                           ORGANISM: Sorghum bicolor FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 72; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 GTGGCGCTGCTCA
                                                                                                       301 TIGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA 360
                                                                                                                                          151 ATGGCGGCGCCTACTACGGCGGAGGCCCTGCGCCACCGGCGGCGGCGGCGCCCCT 210
                                 361 AACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTC 417
                                                                    211 GTGGCGGTGGTGTCCCCCGCAGTTCTGCGCGCCGTACGTGGTGCCCCTGACGGTGACCAAG
                                                                                                                                                                               241 ATGCTGGTCATCGCCCTCGTTGTGGGGCGCAGCGCCCTGGGGCGCCATCGCGCTCACCACA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCATGTGGTCA 358
 AAGGCCATCAGCCTCTCCGACGGCGACTTCACCGTCACCGACGCCAACGGCGCCGTC 327
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ilarity 49.7%;
Conservative
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                                                                                                                                                                                                                                                        Length 1034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11511, Application US/10100683 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: US 60/043,576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PS900
CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: PS900
CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application NUMBER OF SEQ ID NOS: 13468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/056,664
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                          FITLE OF INVENTION: Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/056,892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,632
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/043,314
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APPLICATION NUMBER: US 60/047,599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-08-22
                                                          APPLICATION NUMBER: US 60/056,664 FILING DATE: 1997-08-22
                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/047,601
FILING DATE: 1997-05-23
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                                                                                                                           FILING DATE: APPLICATION
                                                                                                                                                                 APPLICATION NUMBER: US 60/043,580
                                                                                                                                                                                     APPLICATION NUMBER: US 60/056,845 FILING DATE: 1997-08-22
FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,632
                                        APPLICATION NUMBER: US 60/043,314
                                                                                                       FILING DATE:
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75.4%;
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Pred. No. 0.
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; OTHER INFORMATION: Clone ID: US-10-767-701-744
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NUMBER OF SEQ ID NOS: 13468
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11511
LENGTH: 7071
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SEQ ID NO 7545
LENGTH: 666
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                        Sequence 744, Application US/10767701

SEREAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)
CURRENT APPLICATION UNMEER: US/10/767,701
CURRENT APPLICATION ATE: 2004-01-29
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Best Local Similarity
                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 744
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILLING DATE: 2004-01-29
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ORGANISM: Sorghum bicolor
FEATURE:
                                                                                        TYPE: DNA
ORGANISM: Sorghum bicolor
                                                                        FEATURE:
                                                                                                                                                                                ENGTH: 561
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Pred. No. 0.47
0; Mismatches
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                                        SORBI-28MAY03-CLUS124346_1
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Pred. No. 1.
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; ORGANISM: Homo sapiens
US-10-765-790-62
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US-60-548-091-5686
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FILE REFERENCE: 1657/2035
FULE REFERENCE: 1657/2035
CURRENT PLILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: US/10/765,790
CURRENT FILING DATE: 2004-01-27
PRIOR FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 300
SOFTWARE: PatentIn version 3.2
SEQ ID NO 62
LENGTH: 23490
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Best Local
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5686
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GENERAL INFORMATION:
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Local Similarity 49.7%;
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67; Conserv
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Gannon, Allison
Harvey, Jeanne
Lechner, John F.
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Pred. No. 5.7;
0; Mismatches
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Pred. No. 0.
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0.58;
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US-60-548-091-5686
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US-09-804-291A-500
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Best Local
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SEQ ID NO 500
LENGTH: 930
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                                                                                                       587
                                               629
                                                  Tecree
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Sequence 500, Application US/09804291A
GENERAL INFORMATION:
APPLICANT: ZOZULA, SERGEY
TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
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PRIOR FILLING DATE: 2000-04-24
PRIOR APPLICATION NUMBER: 60/207,702
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/213,849
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
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PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/192,033
PRIOR FILING DATE: 2000-03-24
PRIOR PRIOR PRIOR NUMBER: 60/198,474
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
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CURRENT APPLICATION NUMBER: US/09/804,291A
CURRENT FILING DATE: 2001-03-13
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/266,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/230,732
PRIOR FILING DATE: 2000-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17603 TGCTGGTCATCGGCTCCCTGGTGGCTCGCTGGCTCCTGGGGGATTCAGGAGGGGYGGYTTCT 17662
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569 CAAGCCTCTTAGAACTGATGGTCATCCTCTTGGCCGTTGTGACTCTCATGGTTACTCTGG 628
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(1 Similarity 51.9%;
68; Conservative
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                                                                                               ACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGTGGAGCTTGCCTGCTCAGACA 568
                                                                                                                                            AAATAGCGTTTCACTCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGT 526
                                               TGATTCCTTTTGAAATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTTGTCACGCTGA 586
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ilarity 54.0%;
Conservative
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                                                                                                                                                                                                 Score 33.2; DI
Pred. No. 1.4;
0; Mismatches
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Pred. No. 5
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RESULT 12 US-10-021-698A-716

Sequence 716, Application US/10021698A

APPLICANT: KEITH, TIM

RANDALL

INFORMATION:

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APPLICANT: DEL MASTRO, RICHARD
APPLICANT: SIKON, JASON
APPLICANT: SIKON, JASON
APPLICANT: ALLEN, KRISTINA
APPLICANT: PANDIT, SUNIL
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: 2976-4044USI
CURRENT APPLICATION NUMBER: US/10/021,698A
CURRENT FILING DATE: 2001-10-22
PRIOR PRICHE FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/211,749
PRIOR FILLNG DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 6160
SOFTWARE: Patentin 2.1
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Best Local S
Matches 65
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
                                                                      Best Loc
Matches
                                                                                                                                                                                                                      FILE REPERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 19934
LENGTH: 201
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SEQ ID NO 716
                                                                                                             Query Match
                                                                                                                                                            -60-548-091-19934
                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: modified_base
LOCATION: (88987)..(89086)
OTHER_INFORMATION: a, t, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: a, t, c or g
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                                                                   y Match 3.1%;
Local Similarity 52.7%;
nes 69; Conservative
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242 TGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCCTGGGCGCCATCGCGCTCACCACAT 301
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65; Conserv
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DUPUIS, JOSEE
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ilarity 55.1%;
Conservative
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Pred. No. 28;
0; Mismatches
                                                                 Score 33; DB 7; Length 201; Pred. No. 0.69; Indels
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                                                                                                                                                                                                                                                                        APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)8
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 9054
LENGTH: 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1938
LENGTH: 201
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.1%;
Best Local Similarity 52.7%;
Matches 69; Conservative
                                                                     Query Match 3.0%;
Best Local Similarity 54.0%;
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9054, Application US/10767701 GENERAL INFORMATION:
                                                                                                                                                                                    OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS73927_1
                                                                                                                                                                                                       ORGANISM: Sorghum bicolor FEATURE:
                                                                                                                                                                                                                                                         TYPE: DNA
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609 AAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTTGTGGGTAAT 668
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                                                                  Score 32.8; DI
Pred. No. 2;
0; Mismatches
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Search Job tir	Db	γŞ	g D	Ş	Дb
Search completed: April 17, 2004, 20:12:57 Job time : 126.34 secs	866 GTCC 869	729 CTTC 732	806 GCCCACATGACGCCACTGCCGGTGTTGCTGCTGTGGCTGTGGTGCCCATCGTGAA 865	669 TCCAGGTCAGGCCCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACCATCCGGTA 728	746 ATAGCCGTTGCCCTGCTTGCTGCTGCTGTCTTGCTGTCCCATTGCACCCGTAGTGGT 805

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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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AI138160	CG449978	BZ644270	CG449984	CG250542	CC170529	BX384405	BQ678281	CG358991	BX331708	CC669295	BJ287010	BJ525053	CNS00CT2	BE013856	CNS016BR	BH805539	BI586164	B1641382	AI238135	52	8	AI258415	5	BF101158	BG845919	BX382084	8	AJ449936	ໝ	8	CB657749	BX361080	CNS0091P	BF341287	BX425603	W600	U44	C6849	9746	BX540413	
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NO.	Score	Query Match	Query Match Length DB ID	BB	ID .	Description
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N	45	4.2	1201	13	BX356664	BX356664 BX356664
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4.	40.2	3.7	1201	13	BX376097	BX376097 BX376097

RESULT 1
AQ936633
LOCUS
DEFINITION TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT SOURCE ORGANISM ACCESSION VERSION KEYWORDS REFERENCE AUTHORS Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 473)

Zabarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovska,V.V.,

Ziabarovsky,O.V., Kozyrev,S., Petrenko,L., Skobeleva,N.,

Li,J., Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and

Wahlestedt,C.

Wahlestedt,C. Contact: Podowski RM Center for Genomics Research Karolinska Institute 1717 Stockholm, Sweden Tel: +46-8-728-6372 AQ936633 A73 bp DNA linear GSS 23-AUG-2000 HSJ41-905 Human NotI clones Homo sapiens genomic, genomic survey AQ936633.1 GI:7213011 Homo sapiens (human) sequence. 10710430 Fax: +46-8-337983

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AUTHORS
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                                                                     Local Similarity
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Class:
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BX356664 BX356664 BX356664 BX356664 BX356664 BX356664 BX356664 BX356664 BX356664.1 GI:30378083
                                                                                                                                                                                                                                                                                                                                                                  BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODI015CA02NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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 STBSTSSTTSTBTSCTTTBSSTTBYTBSSSBSBSSBTTSSCSCTSSBSTTSSTBSMTSS
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                                   GTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGG
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NotI site.
                                                                                                                                                        /tissue_type="PLACENTA COT 25-NORWALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
/note="Tist strand cDNA was primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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mol_type="genomic DNA"

db_xref="taxon:9606"
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/clone="CS0DI015YB03"
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                                                                     Score 45; DB 1
Pred. No. 0.65;
68; Mismatches
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                                                                                                     DB 13; Length 1201;
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                                                                         148;
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                                        17; Conserv
                                                                                                                                                                                                                                                                                                                                                                              Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com |
http://fullength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO72CCO3NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Gatarrhini; Hominidae; Homo.

1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Be 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAAACCCCATTGCCCGTTTCTATTCGGT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTS 1107
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CACATTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGT 356
                                 3.8%; Score 40.8; DB 13;
llarity 3.0%; Pred. No. 9.4;
Conservative 191; Mismatches 362;
                                                                                                                                          /tissue type="PIACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PIACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO72YF05"
                                             Indels
                                                                                   Length 1201;
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SOURCE
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                                                                                                                                                                                                                                                                                     BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2866.f
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODC022BG06QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hor 1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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BX376097
BX376097.1 GI:30434756
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               /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED" /Clone_Tib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED" /note="ist strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                           /mol_type= ".....9606"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                     /clone="CSODC022YM12"
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Homo sapiens
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                           TTGGCGCTGGCACCATCGTTTTTGTTGGACTGGTGAATCTTT
                                                                                      TTGCCGTTGCGATTACAGTGGTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCG
                                                                                                                     KKNWMCKAMMCACKKKBCCCYKCBKKKCCCKCCKACCMCCKKKMKKKKAMKKKKKCKKKKKKK
                                                                                                                                                                                 TTTTCBNKKAMKMBKKNKKMCDKAMCNCMAKAKDMKKKMKAKAMKKHANCKKK--CKKMC
                                                                                                                                                                                                           GTGAATCACAATTTGTGGGCAAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTT
                                                                                                                                                                                                                                             KDKACKYCKKYCACKKACKKAMCKNYNIKDMCTWICTMITTITTCTTITTTTCCCCTHTTT
                                                                                                                                                                                                                                                                        TATGTGCAGTCATTACTTTTGCGCTCCGGGCGGTTCCGTTCTTAATCCTTAAGCCCCCTAC
                                                                                                                                                                                                                                                                                                       KKAMMCKKAKAKKKACAKAKAKMIMKKTKKNIMCKMKKKKMCMKKKKKKKKKKKBIMKA
                                                                                                                                                                                                                                                                                                                                     TTCTTGGGAAAGGCTGCTAAATGACAACTGATTTCTCCTGTATTCTCCTTGTTGTCGCAG
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                                                                                                                                                   TGACCGCATCAACGTTTCGCAGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCA
KKBKBKKDMCKKKKKCAKKKRNKKKKKMKKKKMKKKCMBKKKKKKKKKKKKKAMAMKWMANAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 231; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40.2;
Pred. No. 14
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                                                                                                                                                                                                                                                                                                            740
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EX540413/c
                                                             JOURNAL COMMENT
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KEYWORDS
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                                                                                                                                                         REFERENCE
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                                                                                                            TITLE
                                                                                                                                          AUTHORS
65, rue de Saint-Brieuc, Ri
Tel: +33 (0) 2.23.48.54.63
Fax: +33 (0) 2.23.48.54.70
                                                                                           Klopp, C. and Douaire, M. Construction and primary characterization multi-tissue cDNA libraries
                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                       Gallus gallus
Gallus gallus
                                                                                                                                                                                                                                                     BX540413.1 GI:33294986
EST.
                                                                                                                                                                                                                                                                                               BX540413
BX540413 AGENAE Gallus gallus multitissues library (9
gallus cDNA clone gcab0001b.d.10 Sprim, mRNA sequence.
                                                             Unpublished (2003)
Contact: Douaire M
                                                                                                                                                                                                                                                                                     gallus cDNA
BX540413
                                                                                                                                         Herault, F.,
                                                                                                                                         (bases 1 to 692) rault, F., Le Meuth-Metzinger, V.,
                                              UMR INRA-ENSAR Genetique
                                                                                                                                                                                                                                      (chicken)
                                   RENNES
                                                Animale
                                 cedex,
                                                                                                                                              Desert, C.,
                                   35042,
                                                                                                                Ġ.
                                                                                                                 chicken
                                                                                                                                              Retout, E.,
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                                                                                                                                                                                                                                                                                                                   (gcab)
                                                                                                                normalized
                                                                                                                                                                                                                                                                                                                        Gallus
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Email: Madeleine.Douaire@roazhon.inra.fr Sequence cleaned of vector, adaptator and re at sigenasupport@jouy.inra.fr to obtain the

repetitions. Contact us he chromatogram of this

FEATURES

Plate: 0001 row: Seq primer: M13R.

row: d

column:

Location/Qualifiers

.692

sequence.

source

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AJ397466/c
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           718 bp
AJ397466 dkfz426 Gallus gallus c
AJ397466 dkfz426 Gallus gallus c
AJ397466.1 GI:7130433
EST.
                                                                                                                                                                                                                                                                                                                                                                                            Abdrakhmanov,I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy,J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                           Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 2025! Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 718)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTGCTAAGGTCACCTTCTTGCTGCAGCCTCTGCAG 225
                                                    tissue_type="Bursa of Fabricius"
/cell type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/clone_lib="dkfz426"
                                                                                                                                                                                    /organism="Gallus gallus"
/mol_type="mRNA"
                                                                                                                                                     db_xref="taxon:9031"
                                                                                                                                   clone="217r1"
    .7%;
    Score 39.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA clone 217r1, mRNA sequence.
      BB
      9
    Length 718;
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BU448643 1756 bp mRNA linear EST 29-NOV-2002 603211326F1 CSEQRBN13 Gallus gallus cDNA clone ChEST191c7 5', mRNA

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CC684922
LOCUS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 CTTGGGGGCAGTTGGCCATCTGCTCCTGCACCTTTGCACAAGACGAGACGTGAGACCGCAT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 705 CTTGGGTCTGTTGACCATCCGGTACTTCTTCTTGGGAAAGGCTGCTAAATGACAACTGAT
                                                                                                                                                                       535 GTTTCGCGGCGGCCACCCGGATCCAGCTCGGGCTTCGCGAGCGCCTCTAAAGCTTCAGGTC
                                                                                                                                                                                                                                           475 CCTCCGCCTCCGCGCCGTTCCGTCCTCCACTCCTCATCTCGCGATTGGCAAATTCTAGG
                                                                                                        595
                                                                                                                                       551 TCGAGTTCGCCCTTTGCTCTCTTTGTCACGC 583
                                                                                                                                                                                                          491 TATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAAATTAAGGGCC
                                                                                                                                                                                                                                                                          431 CCGCAGGCTGGTCGGCGAGCTTATCTCAATGCAAATAGCGTTTCACTCCTACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Liliopsida; Poales; Poaceae; PACCAD
spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
loade; Panicoideae; Andropogoneae; Zea.
loade; Paccas 1 to 743
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
                                                                                                                                                                                                                                                                                                               82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC684922 743 bp DNA linear GSS 19-JU OGUAX55TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0397J14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence.
CC684922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other_GSSs: OGUAX55TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC684922.1
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                                                                                                                                                                                                                                                                                                             3.7%;
ilarity 53.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4577"
/clone="zMMBMa0397J14"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK.; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:32089698
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rrcrccrerarrcrccrrerrercecaerarerecae 801

Best Loc Matches

61;

Conservative

0

705

сттеретствательност статем под применения при

/notes"Vector: pT7T3D-pac; Clone distribution : AGENAE Resource centre. François PIUMI, François.Piumi.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"

/tissue_type="adipose tissue, granulosa, multi-tissues, oviduct, small folicule, utero-vaginal gland" /dev_stage="adult" /lab_host="DH10B"

/clone lib="AGENAE Gallus gallus multi-tissues library

/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="gcab0001b.d.10"

organism="Gallus gallus"

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262

Local

Similarity

3.7%;

Score 39.4; DI Pred. No. 17; 0; Mismatches

DB 13;

Length

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Query Match

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1 (bases 1 to 756)

2 (bases 1 to 756)

3 (bases 1 to 756)

4 (bases 1 to 756)

4 (bases 1 to 756)

5 (bases 1 to 756)

6 (bases 1 to 756)

7 (bases 1 to 756)

8 (bases 1 to 756)

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8 (bases 1 to 756)

9 (bases 1 to 756)

9 (bases 1 to 756)

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Gallus gallus
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Tel: 01612008930
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                                                                               Drosophila melanogaster genome BACR20K04 of RPCI-98 library fifly), genomic survey sequence.
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fly), genomic survey s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="forgan: ovary; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: Not1; This normalized library was constructed_from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was mormalized in 2 rounds using conditions adapted from Soares et al., PNAS conditions adapted from Soares et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1994) 91: 9228-9232 and Bonaldo et al., Genome Research (1996): 791, except that a significantly longer reannealing hybridization was used."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9031"
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/mol_type="mRNA"
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Pred. No. 18;
0; Mismatches
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                                                                                                                                                                       787 bp
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survey sequence T7 end of BAC #
rom Drosophila melanogaster (fruit
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                                                                                                          Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Primates; Catarrhini; Ho
1 (bases 1 to 885)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                 Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                        Contact: Genoscope
         Email: seqref@genoscope.cns.fr,
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 612 GCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTTGTGGTAATTCC
                                                                                                                                                                                                                                                                     214 TAATTTCGCCATATGGTTATATCGGATTTTTTTTTATTGGTCCGCTGA 168
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Edopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.f:
                               885 bp mRNA
BX42503 Homo sapiens NEUROBLASTOWA Homo
CLOBB022ZA07 3-PRIME, mRNA sequence
BX425603
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BX425603.1 GI:30770486
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BARR20X04"
/clone="BARR20X04"
/note="end : T7"
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

Web : www.genoscope.cns

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com | http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CLOBB022ZA07FP1.
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 859)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1999)
                                                                                                                                                                               602013222F1 NCI_CGAP_Brn64 Homo
5', mRNA secritoria
                                                                                                                                                             5', mRNA sequence.
BF341287
 Contact:
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                                                                                                                   Homo sapiens (human)
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llarity 1.5%;
Conservative 14
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/clone_Tib="Homo sapiens NEUROBLASTOMA"
/clone_Tib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pc/WYSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned i
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
Robert Strausberg,
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/mol_type="mRNA"
/db_xref="taxon:9606"
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s; Pred. No. 20;
147; Mismatches 323;
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NA clone
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
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90; Conserv
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Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9410 row: k column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNS0091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSD
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llarity 51.4%;
Conservative
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/lab_host="PH10B (TI phage-resistant)"
/clone lib="NCI (GAP_Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size_1.57 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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/db_xref="taxon:9606"
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Pred. No. 25;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                    National de Sequencage : seqref@genoscope.cns.fr
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BX361080
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Matches 37
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                                                                                                                                                                    Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com |
http://fulllength.invitrogen.com/ InVitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO79DG08NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX361080
1201 bp mRNA linear EST 05-MAY-200
BX361080 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1079YN16 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                          Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1201)
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BP 191 91006 EVRY cedex - France
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|mol type="genomic DNA"
|db xref="taxon:7227"
|/clone="BACR19D16"
|/clone lib="RPCI-98"
|/note="end : TET3"
                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI079YN16"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Jst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
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14.2%; Pred. No. 26;
tive 117; Mismatches 106;
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Query Match
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                                       CACGTATTCTATGCGTTTTCATT 341
                                                                              GTTGTGGGCGCAGCGCCCTGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTTCCGC
                                                                                                                                                                KADNIMIMIMIKKKOMIKOMIKOKKKOMIMIKKOOMIMIKKOO KHINIKIMIKKKKOMIMIKKK 1064
                                                                                                                                                                                                     GCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTC
                                                                                                                                                                                                                                              KKKKKKKKKTTTTWTTTTTTHTTMTMMHTTTTTTMMTTTTTHNKKKKKKKKKK 1004
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CCCKKKKKBCKKKKKKKCCCKKK 1147
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Pred. No. 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 142;
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OSJNEC13F02.f OSJNEC Oryza sativa (japonica clone OSJNEC13F02.5', mRNA sequence. CB657749 CB657749.1 GI:29661474
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Unpublished (2003)
                                                                                                                                                            Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                                                                                                                                        FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat
Plate: 13 row: F column: 02
                                                                                                                                                                                                                                                                                              Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                              PCR PRimers
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Biological Sciences W
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/organism="Oryza sativa (japonica 
/mol type="mRNA" 
/culTivar="Nipponbare" 
/db xref="taxon:39947" 
/clone="OSJNEC13F02" 
/tissue_type="Leaf"
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Query Match 3.5%; Score 37.8; I Best Local Similarity 34.0%; Pred. No. 57; Matches 54; Conservative 41; Mismatches
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AL060428
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GSS.
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Submitted (02-UN-1999) Genoscope - Centre National de Sequencage :
BP 191006 EVRY Cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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/lab_host="DHIOB"
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/clome_lib="OSJNEG"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 6 hrs after innoculation with Rice_Blast (C9240-1)"
                                                                                                                                                                                                              /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db xref="taxon:7227"
/clone="BACR12G04"
/clone_lib="RPCI-98"
/note="end : TET3"
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Pred. No. is the number of results predicted by chance to have

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SUMMARIES

Result No. 0000 Ω O 00000 n a a O a 273.6 273.6 149.6 132.6 127.4 127.4 127.4 Score 59.85 59.85 57.68 54.4 68.65 Query Match 100. 1000. 1000. 1000. 1000. 1000. 1000. 1000. 1000. 1000. 1000. 1000. 1000. 1000. 1000. 1000. 1000. 1000. 1000. 1000. 7.9 349926 7.9 349926 7.8 9888 7.2 9888 7.2 9888 7.2 10733 7.3 2000 7.4 30183 7.5 2 10733 7.6 2 20050 7.7 20050 7.7 20050 7.8 30050 . . . 711 309400 325651 715 715 Length 87340 53793 711 띪 AR391954 ARX137710 BD014992 BD014995 AR391956 ARX137710 BD014991 BD014991 BD014991 BD014991 BD014991 BD014991 BD015274 AR7137085 ARX137085 ARX123492 BDX248361 BRX24836284 BRX24836284 BRX24836284 BRX24836286 BRX6404461 BRX6404461 ARE016925 AR391954 Sequence AX137710 Sequence AX137710 Sequence BD014992 Nucleotid BD162490 Novel pol AR291955 Sequence AX137714 Sequence AX137714 Sequence AX137714 Sequence AX137714 Sequence AX137715 Sequence AX137085 Sequence AX137087 Sequence BD01395 Novel nuc BX571660 Woilnella AX137087 Sequence BD01395 Novel nuc BX571660 Woilnella AX386287 Sequence AX011050 Methanosa AX0125448 Homo sapi AX017253 Sequence AX017209 Geobacter AX655393 Sequence AX1174156 Yersinia AX01888 Salmonell BX640441 Bordetell BX640441 Bordetell BX640441 Bordetell BX640426 Mesorhizo AX01584 Salmonell AX016846 Salmonell AX016846 Salmonell AX016846 Salmonell AX016846 Salmonell AX016846 Salmonell Description

ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AR391954	RESULT 1
acids, process for the isolation thereof and use thereof Patent: US 6613545-A 2 02-SEP-2003;	Nucleotide sequences coding for the export of branched chain amino	Kennerknecht, N., Sahm, H., Eggeling, L. and Pieiterle, W.	1 (bases 1 to 753)	Unclassified.	Unknown.	Unknown.	•	AR391954.1 GI:40115725	AR391954	Sequence 2 from patent US 6613545.	AR391954 753 bp DNA linear PAT 18-DEC-2003	•	

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RESULT 2
AX120373
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Bacteria; Actinobacteria; Actinobacteridae;
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/mol_type="genomic
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Patent: ED 1108790-A 289 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
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/db_xref="taxon:1718"
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REFERENCE
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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δλ Β	601 CGAACGAAAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCAGCATAGCTCAT 900 661 GTGGTAATTCCAGGTCAGGCCCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACC 720
8 8 8 8	61 GIGGIANTICCAGGICAGGCCCIATTIGCGCCGCTGATCTTCTTGGGTCTGTTGACC 61 GTGGTAATTCCAGGTCAGGCCCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACC 21 ATCCGGTACTTCTTCTTGGGAAAGGCTGCTAAA 753
RESULT 4 BD014992 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	BD014992 N Nucleotide sequence encoding the discharge of branched amino acid, method of isolating the same and utilization thereof. BD014992 BD014992.1 GI:22555799 JP 2001169788-A/2. unidentified unidentified unidentified
REFERENCE AUTHORS TITLE JOURNAL	
COMMENT	OS COTYMEDACCETIUM GIUCEMICUM AICCL*/52 PN JP 2001169788-A/2 PD 26-JUN-2001 P 2000324315 PF 24-OCT-2909 DE 19951708 8 PI NICOLE KENNERUKUNEHITO, HERWANN SAHM, LOTHAR EGGERING, WALTER PI PFEFFERLE PC (C12N15/09, C07K14/34, C12N1/21, C12P13/06, C12P13/06, C12P13/08//PC (C12N15/09, C12R1:15), (C12N1/21, C12P13/06, C12P13/06, C12R1:15), PC (C12N15/00, C12R1:15) PC (C12N15/00, C12R1:15)
FEATURES sour	FT CDS (1). (7) Location/Qualifiers 1753 /organism="unidentifi /mol_type="genomic Di /db_xref="taxon:3264
Query M Best Lo Matches	/ Match 100.0%; Score 753; DB 6; Length 753; Local Similarity 100.0%; Pred. No. 9.8e-185; Nes 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	61 GAACCAGATGATAAAAGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAACCTCCCTT 120
\$ 8	121 GCTGCAGGTTTGGGCATGTACCCGATTGGTATTTGCGTTTGGTCTCTTGGTTATTCAATAC 180

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UNICLEASE LITEG.

1 (bases 1 to 753)

2E 1 (bases 1 to 753)

RS Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoo, A., Ikeda, M. and Ozaki, A.

Novel polymucleotide

Patent: JP 2002191370-A 289 09-JUL-2002;

KYOWA HAKKO KOGYO CO LTD

OS COTYNEBACTETIUM glutamicum
PN JP 2002191370-A 289

PD 09-JUL-2002

PO 15-DEC-2000 JP 2000405096
PF 15-DEC-2000 
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/db_xref="taxon:32644"
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Kennerknecht,N., Sahm,H., Eggeling,L. and Pfefferle,W.
Nucleotide sequences coding for the export of branched chain
acids, process for the isolation thereof and use thereof
Patent: US 6613545-A 1 02-SEP-2003;
Location/Qualifiers
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Kennerknecht,N., Sahm,H., Eggeling,L. and Pfefferle,W.
Nucleotide sequences coding for the export of branched chain
acids, process for the isolation thereof and use thereof
Patent: US 6613545-A 6 02-SEP-2003;
Cocation/Qualifiers
1. .1271 linear PAT 18-DEC-2003 amino

100.0%; Score 753; DB 6; Length 1271; ilarity 100.0%; Pred. No. 1e-184; Conservative 0; Mismatches 0; Indels 0 0 60 0

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Sequence 1 from Patent EP1096010.
AXI37709
AXI37709.1 GI:14273886
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Nucleotide sequences coding for branched-chain amino acids export
proteins, method for isolating them and their use
Patent: EP 1096010-A 1 02-MAY-2001;
Degussa AG (DE); FORSCHUNGSZENTRUM JUBLICH GMBH (DE)
Location/Qualifiers
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Corynebacterium glutamicum
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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Sequence 6 from Patent EP1096010.
AXI37714
AXI37714.1 GI:14273893
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Degussa AG (DE) ; FORSCHUNGSZENTRUM JUELICH GMBH (DE) LOCALION/Qualifiers
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Corynebacterium glutamicum
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
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                                                                                                                       ATCCGGTACTTCTTCGGGAAAGGCTGCTAAA 753
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Conservative (
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/codon_start=1
/transI_table=11
/protein_id="CAC39928.1"
/db_xref="GI:14273895"
/db_xref="REMTREMBL:CAC39928"
/table=11
/table=114273895"
/table=114273895
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Pred. No. 1e-184;
; Mismatches 0
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discharge
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Best Local Sim:
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Kennerukunehito,N., Sahm,H., Eggering,L. and Pfefferle,W.

Nucleotide sequence encoding the discharge of branched ami
method of isolating the same and utilization thereof
Patent: JP 2001169788-A 1 26-JUN-2001;

POUUSA HUELS AG,FORSCHUNGSZENTRUM JUELICH GMBH
OS COTYNEBACTERIUM GJULTANICH ATCC14752

PN JP 2001169788-A/1

PD 26-JUN-2001

PF 24-OCT-2000 JP 2000324315

PR 27-OCT-1999 DE 1991708.8

PI NICOLE KENNERUKUNEHITO,HERMANN SAHM,LOTHAR EGGERING,
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Similarity 100.0%; F
53; Conservative 0;
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    TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA
                                                                     GCGGCCAGGCCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC
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24-OCT-2000 JP 2000324315
27-OCT-1999 DE 19951708.8
NICOLE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, WALTER
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brnF
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(101)..(953)
(853)..(1176).
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Pred. No. le-184;
); Mismatches 0
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                                                                                                                                                    Query Match
Best Local Sim:
Matches 753;
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                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                      Nucleotide sequence encoding the discharge of branched amino acid, nucleotide sequence encoding the discharge of branched amino acid, method of isolating the same and utilization thereof patent JP 2001169788-A 426-JUN-2001;

DEGUSSA HUELS AG,FORSCHUNGSZENTRUM JUELICH GMBH

OS COTYNE-BACTETIUM GIUTAMICUM ATCC13032

PN JP 2001169788-A/4

PD 26-JUN-2001

PP 24-OCT-2000 JP 2000324315

PR 27-OCT-1999 DE 19951708.8

PI NICOLE KENNERUKUNEHITO,HERMANN SAHM,LOTHAR EGGERING,WALTER PI PFEFERLE

PC (C12N15/09,C07K14/34,C12N1/21,C12R1:15),(C12P13/06,C12R1:15),

PC (C12N15/00,C12R1:15)

CC brnE

FH Key Location/Qualifiers

FH Key (101). (853)

FT gene (103). (1176).
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JP 2001169788-A/4.
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Nucleotide sequence
method of isolating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGTAATTCCAGGTCAGGCCCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACC
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                                                          GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAACCTCCCTT
                                                                                                                       GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG
   GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 1271)
                                                                                                                                                                                                                                                                                                                                                                                   C12N15/09, C07K14/34, C12N1/21, C12P13/06, C12P13/06, C12P13/08// (C12N15/09, C12R1:15), (C12N1/21, C12R1:15), (C12P13/06, C12R1:15), C12N15/00, C12R1:15)
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                     Location/Qualifiers
(101..(853)
(853)..(1176).
Location/Qualifiers
                                                                                                                                                                                                                              /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                   100.0%;
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e encoding
g the same
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                                                                                                                                                      Score 753; DB 6;
Pred. No. 1e-184;
; Mismatches 0;
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and
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Corynebacterium glutamicu regulator (lrp) genes, cc AF454053
AF454053,1 GI:21311379
                                                                                                                                                                   Eggetling, L.

Export of L-isoleucine from Corynebacterium glutamicum:

two-gene-encoded member of a new translocator family

J. Bacteriol. 184 (14), 3947-3956 (2002)
                                                                                                                                                                                                                                 Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1 (bases 1 to 2105)
Kennerknecht, N., Sahm, H., Yen, M.R., Patek, M., Saier Jr, M.H.
                                                                                                                                                                                                                                                             Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                             2 (bases 1 to 2105)
Kennerknecht,N., Eggeling,L.
Direct Submission
                                                                                Submitted (07-NOV-2001) IBT-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCCGGCCTGATTTTCGCGGGCTCCACCGAA 240
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                                  Location/Qualifiers
1. 2105
    organism="Corynebacterium"
/mol_type="genomic DNA"
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m glutamicum BrnE
) genes, complete (
                                                                                                                and
                                                                                 Forschungszentrum,
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                      glutamicum'
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Leo-Brandt

Str.,

BCT 27-JUN-2002

720

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                       TTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA
                                                                                              ATGCTGGTCATCGCCCTCGTTGTGGGCGCCACCACCCTGGGCGCCCATCGCGCTCACCACA
                                                                                                                                        GGCTACGAATGGTGGGCAGCCCACTGTTTTCCGGGCCTGATTTTCGCGGGCTCCACCGAA
                                                                                                                                                                           GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGGCCTGATTTTCGCGGGCTCCACCGAA 240
                                                                   ATGCTGGTCATCGCCCTCGTTGTGGGCGCGCCAGCGCCCCTGGGCGCCATCGCGCTCACCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MKLDSIDRAIIABLSANARISNLALADKVHLTPGPCLRRVQRLE
AEGIILGYSADIHPAVMNRGFEVTVDVTLSNFDRSTVDNFESSVAQHDEVLELHRLFG
SPDYFVRIGVADLEAYEQFLSSHIQTVPGIAKISSRFAMKVVKPARPQV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MOKTQEIHSSLEVSPSKAALEPDDKGYRRYEIAQGLKTSLAAGL
GMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVYGAAPLAGIALITLL
VNFRRYFYSAFSEPLHTVKNAPLAFSCVIPALDEXYAVVRARPAGWSAWRLISMOIAFH
SYWVFGGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDSCRTKKQIPSLLLAGLSFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAM46685.1"
/db_xref="G1:21311380"
/trans1ation="MTDESCILLVVAVCAVITFALRAVPFLILKPLRESQFVGKMAM
/trans1ation="MTDESCILLVVAVCAVITVAHLLGGRRTLLSVGAGTIVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:1718" complement(385. .711)
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complement(708. .1463)
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/trans1_table=11
/product="http-like regulator"
/protein_id="AAM46687.1"
/db_xref="GI:21311382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALVVIPGQALFAALLIFLGLLTIRYFFLGKAAK"
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/transl_table=
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acid export protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11/product="BrnE"
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/transl_table=
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acid export protein"
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|gene="lrp"
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/db_xref="GI:21311381"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 753; DB 1;
Pred. No. 1e-184;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Direct Submission
Submitted (04 MAY-2002) Saboshi Nakagawa, Kyowa Hakko F
Ltd., Tokyo Nesearch Labbylatories; 3-6-6, Asahi-machi,
Tokyo 194-8539, Japan (E-mail:snakagawa@xanagen.com,
Tel:81-44-829-3631, Fax,61-44-013-1651)
This sequence is Conducted by collaboration of Kyowa Hakko Kitasato University.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum ATCC 13032
Corynebacterium glutamicum ATCC 13032
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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AP005274.1 GI:21322764
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Corynebacterium glutamicum ATCC 13032 DNA,
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                   replication
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genome, section
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Hakko Kogyo

initiation"

Kogyo Co. , Machida,

ATCC 13032

xref="GI:21322765"

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gene
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PF02768:DNA polymerase III beta subunit, C-terminal dom
TIGR00663:dnan: DNA polymerase III, beta subunit"
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349980 bp
Sequence 1 from Patent EP1108790.
AX120085 AX114121
AX120085.1 GI:14036800
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Patent: EP 1108790-A 1 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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/mol type="genomic DNA"
/db_xref="taxon:1718"
/note="Seq 1 to long (3.309.400)
0.000.001 0.349.980 349.980"
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1 GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG 0 Score 753; DB 6; 1 Pred. No. 1.2e-184; ; Mismatches 0; Length 349980; <u>.</u> 9 0

276889 GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCGAAGGTCTAAAAAACCTCCCTT GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGGCCTGATTTTCGCGGGCTCCACCGAA GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAA GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC 240 180 276948 120 276888 277068 277008

ANGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCTGGGCGCCATCGCGCTCACCACA ATGCTGGTCATCGCCCTCGTTGTGGGCGCGCAGCGCCCTGGGGCGCCATCGCGCTCACCACA 277128

AACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGAAGCCTACGCAGTCACT AACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT TIGCIGGIGAACTICCGCCACGIATICIAIGCGITTICATICCCGCIGCAIGIGGICAAA TTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA 360 277248 277188

GCGGCCAGGCCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC GCGGCCAGGCCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC 480 540 277308

ATTAAGGGCCTCGAGTTCGCCCTTTTGCTCTCTTTTGTCACGCTGACTTTGGATTCCTGC TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA CGAACGAAAAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTT 660 600 277488 277368 277428

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Search completed: April 19, 2004, 18:29:57 Job time : 3195.51 secs
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Sequence 7 from Patent EP1090993.
AXI37083
AXI37083.1 GI:14273428
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Degussa AG (DE)
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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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/mol_type="unassigned DNA"
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/noTe="1rp-Teil 1"
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This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) polypeptides; (ii) encodes a polypeptide at least 70% identical with (3) or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least 50 consecutive bases from (i)-(iii). The invention also describes (a) protein derived from sequences of 753 bp (2) or 324 bp (4); (b) coryneform microorganisms, especially Corynebacterium, transformed with one or more (I), where these are replicative DNA; (c) production of
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                                                                                                                                                                                                                                                             New export genes from coryneform bacteria, useful for increasing fermentative production of branched-chain amino acids.
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ALIGNMENTS

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L-amino acid production; brnF; coryneform bacterium; leucine; animal nutrition; ds.
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WPI; 2001-391595/42.
P-PSDB; AAB86247.
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FORSCHUNGSZENTRUM JUELICH GMBH.
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isoleucine; valine; medicine;
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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Tateishi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
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                                           GGCTA.CGAATGGTGGGCAGCCCCACTGTTTTCCGGGCCTGATTTTCGCGGGCTCCACCGAA
                                                                                                                                         GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT
ATGCTGGTCATCGCCCTCGTTGTGGGCGCCAGCGCCCTGGGCGCCATCGCGCTCACCACA
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Senoh A,
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                          Kennerknecht N,
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                                                                      (DEGS ) DEGUSSA AG.
(KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
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WPI; 2001-391595/42. P-PSDB; AAB86247, AAB86248

New export genes from coryneform bacteria, useful for increasing fermentative production of branched-chain amino acids.

23pp; German

This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that CC encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) colypeptides; (ii) encodes a polypeptide at least 70% identical with (3) cor (5); (iii) is the complement of (i) or (ii), or (iv) contains at least CC 15 consecutive bases from (i)-(ii). The invention also describes (a) protein derived from sequences of 753 bp (2) or 324 bp (4); (b) cc coryneform microorganisms, especially Corynebacterium, transformed with CC one or more (I), where these are replicative DNA; (c) production of CC one or more (I), where these are replicative DNA; (c) production of CC branched-chain L-aa by fermentation of coryneform bacteria in which the brnE and/or brnF genes (or equivalent sequences) are amplified, coryneform bacteria being considered. (I) is used for transformation of coryneform bacteria being considered for fermentative production of branched-chain amino acide, and corynebacterium medicine corynebacterium strition. (I) can also be used as source of primers and corynebacterium glutamicum ATCC 14752 brnF and brnE proteins described in the corynebacterium glutamicum ATCC 14752 brnF and brnE proteins described in the corynebacterium glutamicum ATCC 14752 brnF and brnE proteins described in the corynebacterium glutamicum ATCC 14752 brnF and brnE proteins described in the corynebacterium glutamicum ATCC 14752 brnF and brnE proteins described in the corynebacterium glutamicum ATCC 14752 brnF and brnE proteins described in method of the invention

Sequence 1271 BP; 265 A; 328 C; 318 G; 360 T; 0 U; 0 Other;

Length 1271;

Query Match

Local

Similarity

밁 S 문 Ś B S 뮍 8 밁 5 片 S 문 Ś 문 S 밁 S Matches 341 221 521 461 361 401 301 241 281 181 121 161 101 GIGCAAAAAACGCAAGAGATICATICAAGCCIGGAGGTGTCGCCATCCAAGGCAGCCCTG 541 481 421 5 1 GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT GCGGCCAGGCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC AACCCCATTGCCCGTTTCTATTCGGTTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT TTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGGCTGCATGTGGGTCAAA ATGCTGGTCATCGCCCTCGTTGTGGGGCGCAGCGCCCCTGGGGCGCCATCGCGCTCACCACA GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAA GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAACCTCCCTT ATTANGGGCCTCGAGTTCGCCCTTTGCTCTCTTTTGTCACGCTGACTTTGGAATTCCTGC TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA AACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT TIGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA ATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCTGGGCGCCATCGCGCTCACCACA GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAA GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC rccracreeerarreeecercreacceeaereecearcecaeaerrearrecritteaa 100.0%; Score 753; DB 4; 1 ilarity 100.0%; Pred. No. 2.5e-223; Conservative 0; Mismatches 0; Indels 0 Gaps 360 300 340 240 160 600 540 580 480 520 420 460 400 280 180 220 120 60 0

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This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that encodes at least one of 251 mmino acid (aa) (3) or 108 aa (5) polypeptides; (ii) encodes a polypeptide at least 70% identical with (3) or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least 15 consecutive bases from (i) - (iii). The invention also describes (a) protein derived from sequences of 753 bp (2) or 324 bp (4); (b) coryneform microorganisms, especially Corynebacterium, transformed with one or more (I), where these are replicative DNA; (c) production of branched-chain I-aa by fermentation of coryneform bacteria in which the especially overexpressed; and (d) method for isolating the brnE and/or brnF genes. (I) is used for transformation of coryneform bacteria being used for fermentative production of branched-chain amino acids,
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                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium. And identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, patticularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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Tateishi
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                                                                                                                                                                                                                                                                                                                               Sequence 349980 BP; 79703 A; 91547 C; 98381 G; 80349 T; 0 U; 0 Other;
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            TTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA
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                                                                                                                                                                                                            GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT
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                                                                  ATGCTGGTCATCGCCCTCGTTGTGGGCGCCAGCGCCCTGGGCGCCATCGCGCTCACCACA
                                                                                            GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAA
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TTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA
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Senoh A,
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2000JP-00159162.
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Pred. No. 3.1e-222;
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Ozaki A;
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ATCCGGTACTTCTTGGGAAAGGCTGCTAAA 277581
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RESULT 6 ACA01969

ACA01969 standard; DNA; 564 E

C ACA01969;

04-JUN-2003 (first entry)

C. glutamicum derived ORF SEQ ID 1960.

Coryneform; nucleic acid array; fermentation; culture; d

DE10128510-A1.

Corynebacterium

glutamicum

19-DEC-2002.

13-JUN-2001; 2001DE-01028510

R 13-JUN-2001; 2001DE-01028510

(DEGS) DEGUSSA AG

Farwick M, Moeckel B, Pfefferle W, Bathe B, Huthmacher K;

WPI; 2003-279970/28

New nucleic acid array useful for monitoring mRNA expression of Corynebacterium glutamicum during fermentation, comprising nucleic acid from Corynebacterium glutamicum.

Claim 1; Page 647; 709pp; German.

This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the invention

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RESULT 7
AAF61693/c
ID AAF61693;
XX
AC AAF61693;
XX
AC AAF61693;
XX
DT 12-UU-200
XX
DF C. glutami
XX
DE C. glutami
XX
M Fermentati
XX
Corynebact
XW Ep1090993.
XX
PN EP1090993.
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PN 11-APR-200
XX
PR 05-OCT-19;
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PR 05-OCT-19;
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PR 05-OCT-19;
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Best Local Similarity
Matches 564; Conserv
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                              05-CCT-1999;
                                                     29-SEP-2000; 2000EP-00121159
                                                                                                        EP1090993-A1
                                                                                                                              Corynebacterium glutamicum
                                                                                                                                                        Fermentation; L-amino medicine; animal feed
                                                                                                                                                                                          C. glutamicum
                                                                                                                                                                                                                     12-JUL-2001
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                                                                                                                                                                                                                                                                    standard; DNA; 397
                                                                                                                                                                                                                                                                                                                                  CTTCTTCTTGGGAAAGGCTGCTAAA 564
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                                                                                                                                                                                          1rp encoding DNA fragment SEQ ID
                              99DE-01047792
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                                                                                                                                                        acid production;
supplement; ds.
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Pred. No. 2.7e-161;
0; Mismatches 0;
                                                                                                                                                                    lrp gene; lysine;
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Best Local Similarity 98.6
Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel isolated nucleic acid (I) from coryneform bacteria used for the fermentative production of selected L-amino acids, by fermenting the amino acid-producing coryneform in which at least the lry gene has been weakened or amplified, then isolating amino acids that have accumulated in the medium or cells. (I) is used to transform coryneforms for production of L-amino acids, specifically lysine and isolatorine, which are used in medicine and particularly as animal feed supplement. It may also be used as probes and primers for isolating related sequences. Regulating expression of (I) improves production of amino acids, especially of L-lysine. This sequence encodes a fragment of the Corynebacterium glutamicum lrp protein which is used in the method described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 397 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 16; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New lrp gene from coryneform bacteria, used to prepare transformants with increased synthesis of amino acids, particularly lysine and isoleucine.
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44
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                   ATGCTGGTCATCGCCCTCGTTGTGGGCGCCAGCGCCCCTGG 280
                                                                                          GCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAA
                                                                                                                                              GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC
                                                                       GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAA
ATGCTGGTCATCGCCCCCGGTTGTGGGCGCACGCCCCGGG
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RESULT 8
AAF61695/c
ID AAF616
Fermentation; L-amino acid production; medicine; animal feed supplement; ds.
                                                                                                               C. glutamicum
                                                                                                                                                AAF61695;
                                                                          Corynebacterium
                                                                                                                              12-JUL-2001 (first entry)
                                                                                                                                                               AAF61695 standard; DNA;
                           29-SEP-2000;
                                           11-APR-2001.
                            2000EP-00121159
                                                                                                                lrp encoding DNA fragment SEQ
            99DE-01047792
                                                                           glutamicum
                                                                                                                                                               778
                                                                                                                                                               ₽₽
                                                                                                lrp gene; lysine; isoleucine;
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(DEGS) DEGUSSA-HUELS

AG.

(DEGS) DEGUSSA-HUELS

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RESULT 9
AAH68373
ID AAH683
ID AAH68
XX AAH6
XX AAH6
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XX CO1
DE C 91
XX CO1
XX CO2
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Best Local S
Matches 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel isolated nucleic acid (1) from coryneform bacteria used for the fermentative production of selected L-amino acids, by fermenting the amino acid-producing coryneform in which at least the lry gene has been weakened or amplified, then isolating amino acids that have accumulated in the medium or cells. (1) is used to transform coryneforms for production of L-amino acids, specifically lysine and isolaucine, which are used in medicine and particularly as animal feed supplement. It may also be used as probes and primers for isolating related sequences. Regulating expression of (1) improves production of amino acids, especially of L-lysine. This sequence encodes a fragment of the Corynebacterium glutamicum lrp protein which is used in the method described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 17; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moeckel
                                                                                                                                                                                                                                                                                           Coryneform bacterium; organic acid synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH68373
                                                                               18-DEC-2000; 2000BP-00127688
                                                                                                                                                                                                                                                                                                                                                                          glutamicum coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     778 BP; 175 A; 208 C; 207 G; 188 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTACGAATGGTGGGCAGCCCACTGTTTTCCGGCCTGATTTTCGCGGGGCTCCACCGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                          amino acid
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Pred. No. 2.3e
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                                                                                                                                                                                                                                                                                                                                                                             fragment SEQ ID NO: 3408.
                                                                                                                                                                                                                                                                                                                             synthesis;
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16-DEC-1999; 99JP-00377484. 07-APR-2000; 2000JP-00159162.

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599 473

658

532 598

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TCAAAAATAACAAGGATTATTCGCTGCCATTATTCGCGGTGGTATTGGCTCTGGTTTCCG

AAATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTTGTCACGCTGACTTTGGATTTCCT

472

659

TIGIGGIAATICCAGGICAGGCCCTATITIGCGGCGCTGATCTICTIGGGTCTGTTGA

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03-AUG-2000; 2000JP-00280988
                                                             AAG93154
                                                                     Mizoguchi H, Au
Senoh A, Ikeda
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                                                                     Ando S, Hayashi M,
da M, Ozaki A;
                                                                         Ochiai K,
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Novel polynuclectides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene

Claim 8; SEQ ID NO 3408; 246pp + Sequence Listing; English.

The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office Sequence 711 BP; 123 A; 190 C; 198 G; 200 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                              GTTTCGCCTGGTGGTGGACGCCGATTTTCTCCTTCGTGATCTATGCCGGTTCGATGGAAT
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    ACTCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTG
                                     CAGCCCGCCCACCTGGCGATATCAGTGGCACGCGGGTGCTTACCGTTCAAATTTTGTGCC
                                                                                                                                                         TCATGGTGAATTTCCGCCACATTTTCTACGGTCTCACCTTCCCACGCCACCGCATCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  16.9%;
                                                                                                                                                                                                                                                                                                                                                                                                  Score 127.4; DB 5;
Pred. No. 6.3e-29;
0; Mismatches 296;
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Best Local Similarity
Matches 318; Conserv
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                                                                                                                                                                                                                                                                                    This invention describes a novel nucleic acid array involving Corynabacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACA01294;
                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid array useful for Corynebacterium glutamicum during from Corynebacterium glutamicum.
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                                                                                                                                                                                                                                                   Sequence 711
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 456; 709pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glutamicum derived ORF SEQ ID
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                TGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAA
                                                 TTCTGGCAATCGGCATGGTCACCGCAGGTATCGGCCGTTTTCGGCGGCGGTCGCTGGTT
                                                                        TGCTGGTCATCGCCTCGTTGTGGGCGCCAGCGCCCCTGGGGCGCATCGCGCTCACCACAT
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TCATGGTGAATTTCCGCCACATTTTCTACGGTCTCACCTTCCCACGCCACCGCATCAAGT
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                                                                                                                                                                                                    o,
                                                                                                                                                                                                    Score 127.4; DB 7;
Pred. No. 6.3e-29;
); Mismatches 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fermentation; culture;
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on, comprising nucleic acid
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ARESULT 11
AAH6634/c
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03-AUG-2000;
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Tateishi
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from

Disclosure; SEQ ID NO 7069; 246pp + Sequence Listing;

English.

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Matches 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 309400 BP; 70133 A; 86477 C; 83115 G; 69675 T; 0 U; 0 Other;
   DE10128510-A1
                                   Corynebacterium
                                                                   Coryneform;
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Pred. No. 9.6e-28;
0; Mismatches 296;
                                                                   fermentation;
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                                                                     culture;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Sim
Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to corynebacterium glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
                                                                                                                                                                                         Fermentation; L-amino acid production; medicine; animal feed supplement; ds.
                                                                                                                                                                                                                            C. glutamicum
                                                                                                                                                                                                                                                                         AAF61688;
                                                                                                                                                                                                                                                                                               AAF61688 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid array useful for Corynebacterium glutamicum during from Corynebacterium glutamicum.
                                          EP1090993-A1
                                                                                                                                                                    Corynebacterium
                                                                                                                                                                                                                                                   12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 647; 709pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-279970/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-2001; 2001DE-01028510
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                                                                                                                                key
-35_signal
                                                                                                         -10_signal
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                                                                                                                                                                                                                                                                                                                                                        GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                         GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                      GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 54 A; 40 C; 47 G; 36 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001DE-01028510
                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                           1rp encoding DNA
                                                                                    /*tag= a
88. .93
/*tag= b
151. .615
                                                                                                                                                                    glutamicum
                                                                 product=
                                                                                                                                              location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.1%; Score 106; DB 7;
100.0%; Fred. No. 1.5e-22;
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                                                              "lrp"
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                                                                                                                                                                                                      gene;
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                                                                                                                                                                                                        lysine;
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                                                                                                                                                                                                                                                                                                                                                                                106
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29-SEP-2000; 11-APR-2001.

2000EP-00121159

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel isolated nucleic acid (I) from coryneform bacteria used for the fermentative production of selected L-amino acids, by fermenting the amino acid-producing coryneform in which at least the lrp gene has been weakened or amplified, then isolating amino acids that have accumulated in the medium or cells. (I) is used to transform coryneforms for production of L-amino acids, specifically lysine and isolaucine, which are used in medicine and particularly as animal feed supplement. It may also be used as probes and primers for isolating related sequences. Regulating expression of (I) improves production of amino acids, especially of L-lysine. This sequence encodes the Corynebacterium glutamicum lrp protein which is used in the method
                                Chang H,
Katagiri
                                                                                                                                                                                                                                                                                                               1938/c
ADA71938
                                                                                                                                                                                                                                            Rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 715 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New lrp gene from coryneform increased synthesis of amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-1999;
            WPI; 2003-175290/17
                                                                                         22-JUN-2001; 2001WO-IB001105
                                                                                                                22-JUN-2001; 2001WO-IB001105
                                                                                                                                                              WO2003000898-A1
                                                                                                                                                                                    Oryza sativa
                                                                                                                                                                                                                                                                    20-NOV-2003
                                                                                                                                                                                                                                            gene,
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                                                                    SYNGENTA PARTICIPATIONS
                             ,
(1)
                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCAAAAAACGCAAGAGTTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG
                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                      GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG
                                  Chen W, F, Quan
                                                                                                                                                                                                                                            SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 A; 173 C; 178 G; 198 T; 0 U; 0 Other;
                                                                                                                                                                                                                     infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
                                  ω
                                                                                                                                                                                                                                             5263
                                  Cooper B,
S, Tao Y,
                                                                                                                                                                                                                                                                                                                DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 85;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacteria, used to prepare transformants with acids, particularly lysine and isoleucine.
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                                  Glazebrook J, (Whitham S, Xie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                  e Goff
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FEFEXSKOOODDOODDOXX Identifying at least pathogenic infection bacterial, fungal or gene expression. one gene involved in plant resistance or response for conferring resistance or tolerance to a plant viral infection by determining or detecting plant 0 0

27; SEQ ID NO 5263; 899pp; English.

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

Query Match Best Local S Matches 75

Similarity

10.2%; 328;

Score 47; 1 Pred. No. 0 Mismatches

DB 7; .001; 323;

Length 2000; Indels

11;

Gaps

75;

Conservative

S В Ş S 밁 S 문 S S 밁 Ś ᅜ 밁 밁 \$ 밁 Ś 밁 S გ 밁 498 616 676 479 378 438 248 736 138 8 AAACGCAAGAGTTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTGGAAACCAG HINTER THE PROPERTY OF THE PRO ACTCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTG 538 RCYCWRYATCYWCCCYRKRGWYSRRSMMRTAGKWKMRSWSRWCRSYSWYKMYKKMWKKSY 259 AAAACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCA 418 YMKWKCTWRRCMCYRWGYTMYTTSRSRWMYTGRYKARYTSKRRYMWYKYRKYCWYYYYGM GTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATACGGCTACG RARMSKRRKWAGASMKSCWMYWRGARSMWYSKYSCSAKCCKKTRYMTSSYMSTGMYGMYS ATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAACCTCCCTTGCTGCAG SCAYCSTSSTSRWMSMYYAAKMGMCGSSGMYRMSKSCKMYSKYSSCKYTGSKKCTKRKYY TIGIGGTAATICCAGGICAGGCCCTATITGCGGCGCIGCIGATCTICTIGGGICIGITGA 718 CCKKYCSCCTKYCSYTGYYRYCKWYKYSYYKCYYCYCYWYMSYMRYMMKCMCSRSCSSWM GCCGAACGAAAAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTC AAATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTCTTTGTCACGCTGACTTTGGATTCCT 598 CTGCGGCCAGGCCCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTC 478 SMKYGAKGCYGCKMWTYCSYGYMKWYTYMGSYKYSRCYKYMRMYMYKGWMYMMYYSAYSS CATTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCA YMKCSYMMRYGYCKACKKCCYAMCWKAAYSGMMYWYRKYSKWMRMSTKYMWSMWYKKCR TCATCGCCCT-----AATGGTGGGCAGCCCACTGTTTTCCGGCCTGATTTTCGCGGGGCTCCACCGAAAATGCTGG S--YKSMSWTSKMSYMGKMTCTMYTSMKGSTRRSKMGRWSGMSRMYMRWWKKMRKRKYMR SKWKYMSKSCSMRMTCSSWCSCCYTCYYGAMCWSCCMSMMYMGSCGCYTRGWKWRSKYSM YMSYGWARSSGTWSRSAAKRTYKGYSTSRRAKMMRACRMYSACRRYSRTSYYCGĆSYCGS MMTWYYYYAKYWKYWYKRRGTMSWYGKSYKKKYCTWWCYMKCMRCYRWRKMMRKKTKYSK 319 - CGTTGTGGGCGCAGCGCCCCTGGGCGCCATCGCGCTCACCA 358 499 187 617 677 199 439 298 559 19 79 658 139

CCATCCGGTACTTCTTC

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YCYWSSGYSMWCTSGTY 2

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ID ARAIO5
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XX JP2000
XX JP2000
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Matches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits of cellulose synthetic equipment, that can be used to increase the amount of cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A gene encoding a cellulose synthetic equipment - for the improvement in the amount of cellulose synthesized in a plant body.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cellulose synthase; cellulose production; increase yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene encoding a subunit of cellulose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10732 BP; 3149 A; 1212 C; 2074 G; 2046 T; 0 U; 2251 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAY85179.
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9649 TTSRCTBYSTBTBTTSRCAXCTBDSTSTAKNSTSTYSTTRCTBYSSRSRGYSYCSRSRSR 9590
                                                                                          9709
                                                                                                                                                                                     9769 GYDANSTERYSSRYSSTYSSDSTYSAKYCAKSTTBTBCYYDAYDACYDAYDANCYSSDST
                                                                                                                                                                                                                                                                               9829 SDSTSTYRCSRSDYDATBSDNSTNCCYDASRTBTBSTNCYARCYTBYDARCSRDSTYSSR 9770
                                                                                                                                                                                                                                                                                                                                                                            9889 RGNCYYNSTNCYDASTSDTBYSRCCYTYSYSSTDSTDSTDSTNSTTBSDCYTTTTBSRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9949 RYSSTCNCYSYCCYTSRYSSTTINSTCRCTTYSYNSTTBTBYSYSSTYSSRGYSSRGSDS
                                                                                                                                          502
                                                                                                                                                                                                                                     442
                                             561
                                                                                                                                                                                                                                                                                                                               382 TCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACTGCGGCCAGGCCCGCAGGCTGG 441
                                                                                                                                                                                                                                                                                                                                                                                                                          322 GTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAAACCCCATTGCCCGTTTCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 GTGGGCGCAGCGCCCTGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTTCCGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 5.5%; Score 41.2; DB 3; Length 10732;
l Similarity 14.7%; Pred. No. 0.13;
64; Conservative 182; Mismatches 189; Indels 1;
                                                                                                                                     CTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAAATTAAGGGCCTCG-AGTTCGC 560
                                          YTBYCSRRCCCYYDAYSCSRYDARCYDACYSYSNSTCYDATBTTSRYSTTYSYYSNCYDA
                                                                                                                                                                                                                               TCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCACTCCTACTGGGTATTCGGCGGT 501
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Qy
621 TTCTCTGCTGCTGCTGCAGGTTTGAGCTTTCACCATTGCTCTTGTGGTAATTCCAGGTCAGG
680
9589 CYSCYTDSSTCYSTTYAYSCTTSRGYSYDASRSTSTYSRCTTSTYSYSTTDYSDC 9530
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681 CCTATTTGCGGGCTG 696
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9529 SDYSTTTBNSTYSSDS 9514
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Search completed: April 19, 2004, 11:42:00 Job time : 352.669 secs

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No.
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Perfect score;
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/cgn2_6/ptcdata/2/ina/bCTUS_COMB.seq:*
/cgn2_6/ptcdata/2/ina/backfIles1.seq:*
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US-09-103-840A-2
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Sequence 3205, Ap
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Best Local Similarity 100.0%; 1
Matches 753; Conservative 0;
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ALIGNMENTS

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APPLICANT: KENNERKRECHT, NICOLE
APPLICANT: SAHM, HERMANI
APPLICANT: SGGELLING, LOTHAR
APPLICANT: SGGELLING, LOTHAR
APPLICANT: PFEFFERLE, WALTER
TITLE OF INVENTION: NUCLECTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/265496/MAS
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR REPLICATION NUMBER: DE 199 51 708.8
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 753
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
THAT THE STORE
                                                                                         ; NAME/KEY: CDS; LOCATION: (1).. (753); OTHER INFORMATION: brnf; OTHER INFORMATION: ATCC14752 US-09-471-803A-2
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Score 753; DB 4; Pred. No. 2.2e-231;
                                 Length 753;
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Mismatches

Indels

0

Gaps

0

240 180 180 120 120 60 60

240

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APPLICANT: KENNERKHECHT, NICOLE
APPLICANT: SAHM, HERMANN
APPLICANT: SGGELING, LOTHAR
APPLICANT: PFEFFERLE, WALTER
TITLE OF INVENTION: NUCLECTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/265496/MAS
CURRENT APPLICATION NUMBER: U9/09/471,803A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 1995
PRIOR FILING DATE: 1999-10-27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 1271
                                                                                NAME/KEY: gene
LOCATION: (101)...(853)
COTHER INFORMATION: brnF
NAME/KEY: gene
LOCATION: (853)...(1176)
OTHER INFORMATION: brnE
OTHER INFORMATION: ATCC14752
US-09-471-803A-1
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GENERAL INFORMATION:
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 753; Conservative (
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TYPE: DNA
ORGANISM: Corynebacterium
FEATURE:
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US-09-471-803A-6

; Sequence 6, Application US/09471803A
; Patent No. 661345
; Patent No. 661345
; Patent No. 661345
; Patent INFORMATION:
; APPLICANT: KENNERKNECHT, NICOLE
; APPLICANT: SAHM, HERMANN
; APPLICANT: EGGELING, LOTHAR
; APPLICANT: PREFFERLE, WALTER
; TITLE OF INVENTION: NUCLECTIOE SEQUENCE CODING FOR THE EXPORT OF
; TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
; TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
; TITLE REFERENCE: 21123/265496/MAS
; CURRENT APPLICATION NUMBER: US/09/471,803A
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: DE 199
; PRIOR APPLICATION NUMBER: DE 199
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
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SEQ ID NO 6

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NAME/KEY: Gene
LOCATION: (101)...(853)
OTHER INFORMATION: brnF
NAME/KEY: Gene
LOCATION: (853)...(1176)
OTHER INFORMATION: brnE
OTHER INFORMATION: ATCC13032
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Best Local
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TYPE: DNA
ORGANISM: Corynebacterium
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Pred. No. 2.9e-231;
Mismatches 0;
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RESULT 4 US-09-489-039A-3016

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; Sequence 3016, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
APPLICATI: Gary Breton et. al
iTITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO K
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3016
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3016
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Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
ITITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREEF: 1800 Diagonal Road, Suite 500
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Best Local Simi
Matches 130;
                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
WEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHOLN PACAGE #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335
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EP 91 114 300.6
                                                                                                              US/07/935,313
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Pred. No. 8.6e-09;
0; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 756;
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US-09-107-532A-1266
                                                                                                                                                                                                                                                                                   Sequence 1266, Application.

Sequence 1266, Application.

Patent No. 6583275

PATHENT INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

APPLICANT: Lynn A Doucette-Stamm and David Bush

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

TOTAL TOTAL
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTATCTCAATGCAAATAGCGTTTCACTCCTACTGGGTATTCGGCGGTCTCACCGGAGTGG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGTCACGCTGACTTTGGATTCCTGCCGAACGAAAAAGCAGATCCCT 621
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                                                ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pTZgpt-F1s
                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                             ZIP: 0235
                                                                                                                                                                                                                                                           ITY: Waltham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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NAME/KEY: misc feature;
LOCATION: (B) LOCATION 1...768;
SEQUENCE DESCRIPTION: SEQ ID NO: 1266;
US-09-107-532A-1266
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Best Local
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REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 1266:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: July 2, 1
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: circular MOLECULE TYPE: DNA (geno HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                    167
                                287
                                                                 212
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                                                                                                                                                                                                                                      107 TANANACCICCTIGCIGCAGGITIGGGCAIGIACCCGAITGGTAITGCGITIGGICICI 166
 272
                                                                                                                                                                                                                                                                           104;
                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 768 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                       TCAAAGACACGTTACCGTTTTTCGGTTATATCGGTATTGGACTTGCATTTGGTATCG
                                                                 CTGGTTCTGCCCAATTTATCACAGTCAGCATGCTTGCTAGTCACAGCCCATTGCTTTCCA
                                                                                                                                     TTGGGÀAAGCTGCCGGATTTCATCCACTAGTCGTCACGTTGATGTCCCTGCTGGTCTATG
 regrireredacerriciadreaarreced 302
                             regecereaceacarrecreareaacrrece 317
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                          49.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
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                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                           Score 39.8; DB 4
Pred. No. 0.0092;
                                                                                                                                                                                                                                                                           Mismatches 107;
                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                              Length 768;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                           211
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RESULT 7

US-09-252-991A-11376

US-09-252-991A-11376

; Sequence 11376, Application US/09252991A

; Patent No. 6551795

; Patent No. 6551795

; Patent No. 6551795

; PITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 11376

; LENGTH: 1038

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11418
LENGTH: 1086
Sequence 8976, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: HONERT STS and Encoded Human Profile OF INVENTION: ESTS and Encoded Human Profile Reference: General 1949R2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 8976
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US-09-621-976-8976/c
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US-09-252-991A-11418
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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o. 6551795
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llarity 55.0%;
Conservative
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Pred. No. 0.017;
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                                                                                                       Proteins.
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; ORGANISM: Homo sapiens
US-09-621-976-8976
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US-09-252-991A-3205/c
                                                                               Patent No. 6551795;
GENERAL INFORMATION:
APPLICANT; MARC J. RA
TITLE OF INVENTION: A
TITLE OF INVENTION: A
                                                                                                                                                                                                                  RESULT 11
US-09-252-991A-2761
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Best Local S
Matches 30
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CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 3205

LENGTH: 1140
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                                                                                                                                                                                               Sequence 2761,
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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Local Similarity 58.0%;
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                                                                                                                                                                          761, Application US/09252991A 6551795
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                                                               : J. Rubenfield et al.
ON: NUCLEIC ACID AND AMINO ACII
ON: AERUGINOSA FOR DIAGNOSTICS
107196.136
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Pred. No. 0.1;
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US-09-020-956-12
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INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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SEQ ID NO 2761
LENGTH: 2061
TYPE: DNA
ORGANIEM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-198
CLASSIFICATION:
OP-FEB-198
CLASSIFICATION UMBER: 31,392
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 65; Conserv
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Best Local Similarity
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
APPLICANT: DIVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-07-27
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     TCGCGCTCACCACATTGCTGGTGAACTTCCGCCACGT 323
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                                                                                                         Score 36.4; DI
Pred. No. 0.11
0; Mismatches
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Pred. No. 0.14;
0; Mismatches 47; Indels 0
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                                                                                                                                           DB 3;
                                                                                                           39;
                                                                                                                                           Length 751;
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RESULT 14

US-09-439-313-12/c

Sequence 12, Application US/09439313
Patent No. 6329505

INFORMATION:

APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin APPLICANT: Mitcham, Jenni APPLICANT: Harlocker, Su APPLICANT: Jiang Yuqui

Dillon, Davin C. Mitcham, Jennifer Harlocker, Susan Louise

Fanger, Gary Retter, Mark Solk, John Reed, Steven G. Kalos, Michael

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RESULT 13
US-09-030-607-12/c
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; MOLECULE TYPE:
US-09-030-607-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/030,607

FILING DATE: 25-FEB-1998

CLASSIFICATION:
                                                                                                                                                   Matches
                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDENUES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
STREET: 63
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59.8%;
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RESULT 15

US-09-352-616A-12/c

; Sequence 12, Application US/09352616A

; Patent No. 6395278

; GENERAL INFORMATION:
    APPLICANT: Dillon, Davin C.
    APPLICANT: Harlocker, Susan Louise
    APPLICANT: Viang, Yuqui
    APPLICANT: Xu, Jiangchun
    APPLICANT: Mitcham, Jennifer Lynn
    APPLICANT: NITCHAM, Jennifer Lynn
    APPLICANT: Mitcham, Jennifer Lynn
    APPLICANT: NITCHAM, Jennifer Lynn
    APPLICANT: NITCHAM, Jennifer Lynn
    APPLICANT: NITCHAM, Jennifer Lynn
    APPLICANT: NITCHAM, Jennifer Lynn
    APPLICANT: Mitcham, Jennifer Lynn
    APPLICANT: NITCHAM, Jennifer Lynn
    APPLICANT:
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FITTLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CUURENT APPLICATION NUMBER: US/09/439,313
CUURENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 751
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(751)
OTHER INFORMATION: n = A,T,C or G
US-09-439-313-12
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; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-12
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Search completed: April 19, 2004, 18:38:14 Job time \cdot 68 4023 secs

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| (cgn2_6/ptodata/1/pna/Us07_NEW_COMB.seq:*
| (cgn2_6/ptodata/1/pna/Us08_NEW_COMB.seq:*
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US-10-767-701-744
US-10-767-701-744
US-10-765-790-62
US-60-548-091-934
US-60-548-091-19934
US-60-548-091-19934
US-60-548-091-19934
US-10-767-701-2054
US-10-767-701-2054
US-10-767-701-30189
US-10-767-701-30189
US-10-775-920-136
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Sequence 10854, Apsequence 5263, Apsequence 5263, Appsequence 10866, Apsequence 11511, Apsequence 62, Appl Sequence 62, Appl Sequence 62, Appl Sequence 5686, Apsequence 5686, Apsequence 1993, Apsequence 1993, Asequence 2018, Apsequence 2189, Apsequence 14711, Asequence 136, Appsequence 136, Appsequence 136, Appsequence 459, Appsequence 459, Appsequence 458, Appsequence 131, App
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31.4 4.2 596 6 US-10-767-701-19807 Sequence 8, 43 31.4 4.2 3147 6 US-10-763-450-8 Sequence 8, 44 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8, 45 31.4 4.2 3379 1 PCT-IL04-00078-35 Sequence 35	38 32 4.2 32644 6 US-10-796-307-8771 Sequence 87 39 32 4.2 84156 6 US-10-796-307-8770 Sequence 87 40 31.6 4.2 715 6 US-10-767-701-3886 Sequence 38 41 31.6 4.2 5448 1 PCT-US03-38685-2 42 31.4 4.2 596 6 US-10-767-701-19807 Sequence 29 43 31.4 4.2 3147 6 US-10-763-450-8 44 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8, 45 31.4 4.2 3379 1 PCT-IL04-00078-35 Sequence 35	37 32 4.2 1271 6 US-10-796-307-259 Sequence 27 38 32 4.2 32644 6 US-10-796-307-8771 Sequence 87 39 32 4.2 84156 6 US-10-796-307-8770 Sequence 87 40 31.6 4.2 715 6 US-10-767-701-9886 Sequence 2, 41 31.6 4.2 5448 1 PCT-US03-38685-2 Sequence 2, 42 31.4 4.2 596 6 US-10-767-701-19807 Sequence 1, 43 31.4 4.2 3147 6 US-10-763-450-8 Sequence 8, 44 31.4 4.2 3147 6 US-10-763-450-8 Sequence 8, 45 31.4 4.2 3147 6 US-10-769-565-8 Sequence 35	36 32 4.2 1202 6 US-10-796-307-258 Sequence 25 37 32 4.2 1271 6 US-10-796-307-259 Sequence 25 38 32 4.2 32644 6 US-10-796-307-8771 Sequence 87 39 32 4.2 32644 6 US-10-796-307-8770 Sequence 87 30 31.6 4.2 715 6 US-10-767-701-3886 Sequence 38 41 31.6 4.2 5448 1 PCT-US03-28685-2 Sequence 2, 42 31.4 4.2 548 0 US-10-767-701-19807 Sequence 8, 43 31.4 4.2 3147 6 US-10-763-450-8 Sequence 8, 44 31.4 4.2 3147 6 US-10-763-450-8 Sequence 8, 45 31.4 4.2 3379 1 PCT-IL04-00078-35 Sequence 35	35 32.2 4.3 228854 7 US-60-548-091-5633 Sequence 25 36 32 4.2 1202 6 US-10-796-307-258 Sequence 25 37 32 4.2 1271 6 US-10-796-307-259 Sequence 25 38 32 4.2 32644 6 US-10-796-307-8770 Sequence 87 39 32 4.2 32644 6 US-10-796-307-8770 Sequence 87 40 31.6 4.2 715 6 US-10-767-701-3886 Sequence 38 41 31.6 4.2 5448 1 PCT-US03-38685-2 Sequence 2, 42 31.4 4.2 596 6 US-10-767-701-19807 Sequence 8, 43 31.4 4.2 3147 6 US-10-767-701-807 Sequence 8, 44 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8, 45 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8, 46 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8, 47 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8, 48 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8, 49 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8,	34 32.4 4.3 2772 1 PCT US04-07467-29 Sequence 25 32 4.2 1202 6 US-10-796-307-259 Sequence 25 32 4.2 1202 6 US-10-796-307-259 Sequence 25 32 4.2 1271 6 US-10-796-307-259 Sequence 25 32 4.2 3244 6 US-10-796-307-8771 Sequence 27 32 4.2 32644 6 US-10-796-307-8770 Sequence 87 32 4.2 84156 6 US-10-796-307-8770 Sequence 87 31.6 4.2 715 6 US-10-767-701-9886 Sequence 25 31.4 4.2 3147 6 US-10-767-701-19807 Sequence 19 31.4 4.2 3147 6 US-10-763-450-8 Sequence 19 31.4 4.2 3147 6 US-10-763-450-8 Sequence 87 31.4 4.2 3147 6 US-10-763-450-8 Sequence 87 31.4 4.2 3147 6 US-10-769-565-8 Sequence 87 31.4 4.2 3147 6 US-10-769-565-8 Sequence 87 31.4 4.2 3147 6 US-10-769-565-8 Sequence 35 Se	33 32.4 4.3 1625 7 US-60-555-303-460 Sequence 29 34 32.4 4.3 2772 1 PCT-US04-07467-29 Sequence 29 35 32.2 4.3 228854 7 US-60-548-091-563 Sequence 29 36 32 4.2 1202 6 US-10-796-307-258 Sequence 25 37 32 4.2 1216 US-10-796-307-8771 Sequence 25 38 32 4.2 32644 6 US-10-796-307-8771 Sequence 25 38 32 4.2 32644 6 US-10-796-701-3886 40 31.6 4.2 31456 6 US-10-796-307-8770 Sequence 38 41 31.6 4.2 5448 1 PCT-US03-38685-2 Sequence 2, 31.4 4.2 3147 6 US-10-767-701-19807 Sequence 8, 42 31.4 4.2 3147 6 US-10-767-58-8 Sequence 8, 43 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8, 45 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 45 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 46 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 47 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 48 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 49 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 40 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 41 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 42 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 43 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 44 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 45 31.4 4.2 3147 6 US-10-769-565-8 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4.2 715 6 US-10-767-701-3886 Sequence 38 41 31.6 4.2 5448 1 PCT-US03-38685-2 Sequence 2, 42 31.4 4.2 3147 6 US-10-767-701-8077 Sequence 8, 43 31.4 4.2 3147 6 US-10-767-701-8087 Sequence 8, 44 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8, 45 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 46 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 47 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 48 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8, 49 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 49 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 40 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8, 41 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 42 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 43 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 44 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 45 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 46 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 47 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 48 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 49 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 40 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 41 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 42 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 43 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 44 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 45 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 45 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 46 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 47 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 48 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3, 49 31.4 4.2 3147 6 US-10-769-505-30 Sequence 3, 40 31.4 4.2 3147 6 US-10-769-30 Sequence 3, 40 31.4 4.2 3147 6 US-10-76	31 32.4 4.3 1632 7 US-60-553-303-457 Sequence 62: 32 32.4 4.3 1625 7 US-60-553-303-450 Sequence 62: 33 32.4 4.3 1625 7 US-60-553-303-450 Sequence 62: 34 32.4 4.3 1625 7 US-60-553-303-450 Sequence 49: 32 4.3 22854 7 US-60-546-091-563 Sequence 25: 35 32.2 4.3 22854 7 US-60-546-091-563 Sequence 56: 32 4.2 1202 6 US-10-796-307-259 Sequence 25: 36 32 4.2 1202 6 US-10-796-307-877 Sequence 25: 37 32 4.2 32644 6 US-10-796-307-877 Sequence 27: 38 32 4.2 3644 6 US-10-796-307-877 Sequence 87: 39 32 4.2 3644 6 US-10-767-701-886 Sequence 38: 41 31.6 4.2 5448 1 PCT-US03-38685-2 Sequence 19: 42 31.4 4.2 3147 6 US-10-767-763-450 Sequence 19: 43 31.4 4.2 3147 6 US-10-769-565-8 Sequence 81: 44 31.4 4.2 3147 6 US-10-769-565-8 Sequence 81: 45 31.4 4.2 3147 6 US-10-769-565-8 Sequence 35:	30 32.4 4.3 1532 7 US-60-552-390-627 Sequence 45 31 32.4 4.3 1532 7 US-60-552-390-627 Sequence 45 32 32.4 4.3 1625 7 US-60-552-390-625 Sequence 45 33 32.4 4.3 1625 7 US-60-552-390-625 Sequence 62 33 32.4 4.3 1625 7 US-60-552-39.3 460 Sequence 62 34 32.4 4.3 2722 1 PCT-US04-07467-29 Sequence 29 35 32.2 4.3 228854 7 US-60-548-091-563 Sequence 29 36 32 4.2 1272 6 US-10-796-307-258 Sequence 25 37 32 4.2 1272 6 US-10-796-307-8771 Sequence 25 38 32 4.2 1272 6 US-10-796-307-8770 Sequence 27 38 32 4.2 32644 6 US-10-796-307-8770 Sequence 37 39 31.6 4.2 34456 US-10-796-307-8770 Sequence 38 40 31.6 4.2 5448 1 PCT-US03-38865-2 Sequence 29 31.4 4.2 3147 6 US-10-767-701-19807 Sequence 8, 41 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8, 42 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8, 43 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8, 45 31.4 4.2 3147 6 US-10-769-565-8 Sequence 35	29 32.4 4.3 1465 7 US-60-555-303-461 Sequence 62 3 32.4 4.3 1532 7 US-60-555-303-457 Sequence 62 3 32.4 4.3 1532 7 US-60-555-303-457 Sequence 62 3 32.4 4.3 1625 7 US-60-555-303-457 Sequence 45 3 32.4 4.3 1625 7 US-60-555-303-460 Sequence 46 3 32.4 4.3 2772 1 PCT-US04-07467-29 Sequence 29 32.2 4.3 228854 7 US-60-548-091-563 Sequence 29 32.2 4.3 228854 7 US-60-548-091-563 Sequence 25 32 4.2 1202 6 US-10-796-307-259 Sequence 25 37 32 4.2 1271 6 US-10-796-307-8770 Sequence 25 32 4.2 32644 6 US-10-796-307-8770 Sequence 27 31.6 4.2 31.5 6 US-10-796-307-8770 Sequence 87 31.6 4.2 548 1 PCT-US03-38685-2 Sequence 38 4.2 31.4 4.2 31.47 6 US-10-767-701-19807 Sequence 87 31.4 4.2 31.47 6 US-10-767-701-808 Sequence 87 31.4 4.2 31.47 6 US-10-767-701-808 Sequence 87 31.4 4.2 31.47 6 US-10-767-701-808 Sequence 38 Sequence 87 31.4 4.2 31.47 6 US-10-769-565-8 Sequence 31 5 US-10-769-565-8 Sequence	28 32.4 4.3 1465 7 US-60-552-390-623 Sequence 46: 30 32.4 4.3 1435 7 US-60-552-390-627 Sequence 46: 31 32.4 4.3 1532 7 US-60-552-390-627 Sequence 46: 32 32.4 4.3 1532 7 US-60-552-390-627 Sequence 62: 32 32.4 4.3 1625 7 US-60-552-303-457 Sequence 63: 33 32.4 4.3 1625 7 US-60-555-303-450 Sequence 63: 32 4.3 1625 7 US-60-555-303-460 Sequence 29: 34 32.4 4.3 1625 7 US-60-555-303-460 Sequence 29: 35 32.4 4.3 1625 7 US-60-555-303-460 Sequence 29: 36 32 4.2 1202 6 US-10-796-307-259 Sequence 29: 37 32 4.2 1202 6 US-10-796-307-259 Sequence 25: 38 32 4.2 1202 6 US-10-796-307-877 Sequence 25: 39 32 4.2 3244 6 US-10-796-307-877 Sequence 25: 40 31.6 4.2 34456 6 US-10-796-307-877 Sequence 38: 41 31.6 4.2 5448 1 PCT-US03-38685-2 42 31.4 4.2 3147 6 US-10-767-701-1980 Sequence 8: 43 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8: 44 31.4 4.2 3147 6 US-10-769-565-8 Sequence 8: 45 31.4 4.2 3147 6 US-10-769-565-8 Sequence 3:

ALIGNMENTS

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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
ITILE OF INVENTION: Nucleic Acid Molecules and Otl
ITILE OF INVENTION: Plants and Uses Thereof For ITILE OF INVENTION: Plants and Uses Thereof For ITILE OF INVENTION: Plants and Uses Thereof For ITILE OF INVENTION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 10854
LENGTH: 1014
RESULT 2
US-10-417-884A-1266
US-10-417-884A-1266; Application US/1041/...
; Sequence 1266; Application US/1041/...
; GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
; APPLICANT: Lynn A DOUCETTC ACID ENTEROCOCCUS
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.3%;
Best Local Similarity 49.3%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
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and David Bush AND AMINO ACID SEQUENCES RELATING TO FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS

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NAME/KEY: misc feature LOCATION: (B) LOCATION 1...; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-417-884A-1266
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                                                        RESULT 3
US-10-767-701-5263
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APPLICATION UNMER: US/10/417,884A
FILING DATE: 17-Apr-2003
PRIOR APPLICATION DATA:
APPLICATION UNMER: US/09/107,532
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/051571
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
AFTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-8007
TELEPHAN: (781)893-807
INFORMATION FOR SEQ ID NO: 1266:
SEQUENCE CHARACTERISTICS:
Sequence 5263, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RO
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO ORIGINAL SOURCE:
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OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                              TANANACCTCCCTTGCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 768 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                  TTGGGAAAGCTGCCGGATTTCATCCACTAGTCGTCACGTTGATGTCCCTGCTGGTCTATG 211
                                                                                                                                                                                                                                                                                                                      TGGTTATTCAATACGGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCG
                                                                                                                                                                        TCGCGCTCACCACATTGCTGGTGAACTTCCG 317
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ilarity 49.3%;
Conservative
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Pred. No. 0.0082;
0; Mismatches 107;
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226 151 166

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271

RESULT 5 US-10-100-683-983/c

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RESULT 4
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US-10-767-701-5263
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Best Local S
Matches 72
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (5353)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 5263
LENGTH: 619
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 10866
LENGTH: 1034
TYPE: NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10866, Application US/10767701
Sequence 10866, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
CURRENT FILING DATE: 2004-01-29
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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  271
                                  361 AACCCCATTGCCCGTTTCTATTCGGTTTTCGCCGTTATCGACGAAGCCTACGCAGTC 417
                                                                             211 Gregoedriegrerocceccecherrorececceccinaceregrecoccidacegreaccaae
                                                                                                                 301 TŢĢCTĢĢTĢAACŢTÇÇGCÇACGŢAŢTÇTATGÇĢŢTTTCATŢCÇÇGÇŢĢCATĢŢĢGTÇAAA 360
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72; Conservative
                                                                                                                                                                                                                                                          4.6%;
Similarity 49.7%;
                                                                                                                                                          ATGCCGCCCCTACTACGGCGGAGGCCCTGCGCGCGCCACCGGCGGCGGCGGCCCCT 210
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AAGGCCATCAGCCTCTCCGACGGCGACTTCACCGTCACCGACGCCAACGGCGCCGTC 327
                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                            Score 34.6; DB 6; Length 1034; Pred. No. 0.45;
                                                                                                                                                                                                                                           Mismatches
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GENERAL INFORMATION:

Sequence 983, Application US/10100683

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US-10-100-683-983
                                                                                                                                                     PRIOR FILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: US 60/043,576

PRIOR TILING DATE: 1997-04-11

PRIOR APPLICATION NUMBER: US 60/047,601

PRIOR PILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: US 60/056,845

PRIOR FILING DATE: 1997-08-22

PRIOR APPLICATION NUMBER: US 60/043,580

PRIOR APPLICATION NUMBER: US 60/047,599

PRIOR FILING DATE: 1997-04-11

PRIOR APPLICATION NUMBER: US 60/047,599

PRIOR FILING DATE: 1997-05-23

PRIOR FILING DATE: 1997-05-23

PRIOR FILING DATE: 1997-05-23
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LENGTH: 3173
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Best Local Similarity
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PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: US 60/043,576
PRIOR FILING DATE: 1997-04-11
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                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/040,162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen, et al.
TITLE OF INVENTION: Human Secreted Proteins
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APPLICATION NUMBER: US 60/043,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/047,599 FILING DATE: 1997-05-23
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APPLICATION NUMBER: US 60/043,580
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                                   APPLICATION NUMBER: US 60/056,664
PILING DATE: 1997-08-22
APPLICATION NUMBER: US 60/043,314
FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/056,664
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NUMBER: US 60/056,892
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Pred. No. 0.
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APPLICANT: ....alc, David K.

APPLICANT: Cabu, Yihua

ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

ITILE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21 (53535)8

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 744

LENGTH: 561
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FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS92927_1
US-10-767-701-7545
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SEXERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated |
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTON: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTON: NUMBER: US/10/767,701
CURRENT TILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 7545
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11511
LENGTH: 7071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                  ORGANISM: Sorghum bicolor
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS124346_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.6%;
Local Similarity 57.4%;
es 62; Conservative
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43; Conserv
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ilarity 75.4%;
Conservative
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Pred. No. 1.
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US-10-765-790-62
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US-60-548-091-5686
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US-10-765-790-62
Sequence 568, Application US/60548091
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/765,790
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: US 10/737,082
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 300
SOFTWARE: Patentin version 3.2
SEQ ID NO 62
LENGTH: 23490
TYPE- TAXAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 62, Application US/10765790 GENERAL INFORMATION:
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Best Local Similarity
Matches 67; Conserv
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TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
FILE REFERENCE: 1657/2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bayer Healthcare LLC APPLICANT: Beard, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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Gannon, Allison
Harvey, Jeanne
Lechner, John F.
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Pred. No. 3.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
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US-09-804-291A-500
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                                                        CTTTGG 592
                         TGCTGG 634
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; SOFTWARE: PatentIn Ver. 3
; SEQ ID NO 500
; LENGTH: 930
; TYPE: DNA
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-804-291A-500
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; TYPE: DNA
; ORGANISM: Homo s
US-60-548-091-5686
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CURRENT APPLICATION NUMBER: US/09/804,291A
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/188,914
PRIOR FILING DATE: 2000-03-13
PRIOR PILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/198,474
PRIOR APPLICATION NUMBER: 60/198,474
PRIOR APPLICATION NUMBER: 60/199,335
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
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PRIOR APPLICATION NUMBER: 60/207,702
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                                                                                                                                                                                                                                                                                                                                                                                                                  Match 4.4%;
Local Similarity 54.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/226,534
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569 CAAGCCTCTTAGAACTGATGGTCATCCTCTTGGCCGTTGTGACTCTCATGGTTACTCTGG 628
                                                                                                                                                                                                                                                                       467 AAATAGCGTTTCACTCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGT 526
                                                                          TGATTCCTTTTGAAATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTTGTCACGCTGA 586
                                                                                                                                                                                       ACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGTGGAGCTTGCCTGCTCAGACA 568
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Pred. No. 3.9;
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US-60-548-091-19934
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US-60-548-091-19938
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US-60-548-091-19938
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
CURRENT APPLICATION UNMERR: US/60/548,091
CURRENT APPLICATION UNMERR: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19934
LENGTH: 201
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19938
LENGTH: 201
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Best Local Similarity
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RESULT 14 US-10-767-701-9054

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APPLICANT: Kovalic, David K.
APPLICANT: Covalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)8
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ. ID NO 23189
LENGTH: 519
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Best Local S
Matches 67
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53-535) B
FILE REFERENCE: 38-21 (53-535) B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 9054
LENGTH: 1028
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Best Local Similarity 52.6%;
Matches 71; Conservative
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FEATURE:
OTHER INFORMATION: Clone ID: SORBI-2BMAY03-CLUS73927_1
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
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Search completed: April 17, 2004, 20:12:58 Job time: 88.0151 secs

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Maximum DB
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Maximum Match 100%
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                                      Score
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AQ936633
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                                                               SUMMARIES
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AQ936633 HSJ41-905
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Contact: Podowski RM
Center for Genomics Research
Karolinska Institute
17177 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-337983
                                                             Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 473)
Zabarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovska,V.V.,
Xie,L., Muravenko,O.V., Kozycev,S., Petrenko,L., Skobeleva,N.,
Li,J., Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and
Wahlestedt,C.

Woll clones in the analysis of the human genome
Nucleic Acids Res. 28 (7), 1635-1639 (2000)
                                                                                                                                                         AQ936633.1
GSS.
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HSJ41-905 Human NotI clones Homo sapiens genomic, genomic survey
                                                                                                                                                                                                                                                                  GI:7213011
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AL053013 Drosophil
EX361080 EX361080
CB657749 OSJNEC13F
EH887860 LB01712a.
EX382084 EX382084
EB645919 1024011F0
EF101158 601754733
EH80553 1008061A1
AL106545 Drosophil
EB013856 125354 MA
AL05980 Drosophil
EB025053 EJ525053
EJ287010 EJ287010
EX331708 EX331708
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CG358991 OG3AU35TH
EB0678281 AGENCOURT
EX331708 EX331707
CG449984 OGVHO72TV
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EZ366174 OGCEX45TC
CG449978 OGVHO72TV
EZ375719 1e60910.9
CC654373 OGVEL12TV
CG3256716 OGZCO63TV
CG3276716 OGZCO63TV
EX424977 EX424977
AL129189 LP07146.5
CAL09167 SCSGHR106
CF850119 pEM013XA
CC337836 OGTAF14TV
EX359916 EX359916
EX381971 EX381971
CC7865113 DEZ8014XB
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Meb: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com l
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO15CA02NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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/mol_type="mRNA"
/mol_type="mRNA"
/db xref="reaxon:9606"
/db xref="reaxon:9606"
/clone="CSODIOL5YB03"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone="Liype="PLACENTA COT 25-NORMALIZED"
/clone="Liybe="PLACENTA COT 25-NORMALIZED"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 0
                                                                                                                                       Score 45; DB 13; Length 1201; Pred. No. 0.48; Mismatches 148; Indels
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

[ (bases 1 to 743)
whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Numberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2002)
Other_GSSs: OGUAX55TV
                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                               Class: sheared ends.
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                                                                                                                                                     /db_xref="taxon:4577"
/clone="ZMYBMA0397J14"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                /organism="Zea mays"
/mol_type="genomic_DNA"
/strain="B73"
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                                                                  53.6%;
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                                             Score 39.4; DI
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                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffelo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacac.mad wiffelo.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 787)
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AL054013
AL054013.1 GI:4935590
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR20K04 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Direct Submission
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                                                                                             TAATTTCGCCATATGGTTATATCGGATTTTTTTTATTGGTCCGCTGA
                                                                                                                                        AGGICAGGCCTATTTGCGGCGCCTGCTGATCTTCTTGGGTCTGTTGA 718
                                                                                                                                                                                                                        GCAGATCCCTTCTGCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTTGTGGTAATTCC
                                                                                                                                                                                                                                                                                  CTACTTCGTCCTTTCSTCTTTMGTTGTAAMKWGKWWCTTGGAATCCKCTKYAGARARAAC 275
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR20K04"
/clone_lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="end : T7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com l
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO72CCO3NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1201)
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     AAATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCT 598
                                                                                                                                                                                                                                                                                  AAAACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCCTTATCGACGAAGCCTACGCAGTCA 418
                                                                                                                                                                                                                                                                                                                                MMONTONKANMIKKONNMMOMOKAMMOMMIKKONMMMAKKONCOMIKKONCOMIKKKONMIKK 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYNNICNCNKKKKINIKTINMINMYMINININKKKINNINNIKKINNINNINNINNINNIKKMKMSKCKKKKMCCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYWWWCKKWWKKKKKKKKEWSKKWWWWKKYCKWBBWCMSKGGCMMCGCMCKGCVGCMV 1099
                                                                                             ACTCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTG 538
                                                                                                                                             VKKVMCMCDBKMCMCKKKBMKKVCCKKMCMMMMMCAMKVMMMBAMMMMBAMVVMMMMN 1039
                                                                                                                                                                                     CTGCGGCCAGGCCGGCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTC 478
                                                                                                                                                                                                                                        MMMCKKBMMCKKNKMMNKMMVKKKKKAMMNBKĆVMKMKMKMCKKKVMMBKMCAKKKKMCMC 979
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR \
sites of the pCMVSPORT 6 vector. Library was normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI072XF05"
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Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Nammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACGAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1100
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                                                                                                                                                                                                                                                                                                                 638
                                                                                                                                                                                                                                                                                                                                                                                                              37;
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AL053013
AL053013.1 GI:4934461
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoā; Ārthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS0091P
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                                                                                                                                                                                                                                                                                                                                                             GGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGC 254
               YEMBCYTSTSCGGSSSSSGKGGVTKCGCGGCGSSSTNGMBGTSSACSSSSSSSSSSSSSSSSSSSS
                                                                   TTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACTGCGGCCAGGCCCGC 434
                                                                                                                                                                                                                 CCTCGTTGTGGGCGCCAGCCCCCTGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTT 314
                                                                                                                                                                                                                                                                                                            SSSSSTSSSTSSSTSKSSSSGSSSSSSSSSTTSKSTSASGSGSWSAGGGSGSTGSTSS
                                                                                                                 CSCCTCCCSYSYSSSTSSSSSTSWGSTSGSSSSSVGTSSSSDSTSTCCSCCCYMCTCCST 817
                                                                                                                                                                CCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAAAACCCCCATTGCCCG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 925)
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 117; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/mml_type="genomic_DNA"
/db_xref="taxon:7227"
/clone="baCR19D16"
/clone="hBCR19D16"
/clone lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB
Pred. No. 19;
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                       877
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AUTHORS
TITLE
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BX361080
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RESULT 8
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Best Local
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                                                                     1125 CCCKKKKKKBCKKKKKKKKKCCCKKK 1147
                                                                                                                                                                  1065 KKKKKKCCCCBKBCCCCCKYKCCKBKKYCCYKCKKKKKCKKKYCCCBCCCKKKCBCYCC
                                                                                                                                                                                                                                                                1005 KOLDINIMININIMIKKKKAMIKKKKKKKKKKOMMIKKKKAMMIKKKANKHIMIKOMIKIKKKKAMMINIKK 1064
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                                                                                                                 319 CACGTATTCTATGCGTTTTCATT 341
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                                                                                                                                                                                                                 259 GTTGTGGGCGCAGCGCCCTGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTTCCGC 318
                                                                                                                                                                                                                                                                                                            199 GCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTC 258
                                                                                                                                                                                                                                                                                                                                                                  139 TACCCGATTGGTATTGCGTTTGGTCTTGGTTATTCAATACGGCTACGAATGGTGGGCA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                               885 KKKKKDAAKKKKWAKKKKKKAAAAKKKKKKKKKKKKKWWWHEKKKWKKWMKKKKKKDWMKWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 TATCGGCGCTACGAAATCGCGCAAGGTCTAAAAACCTCCCTTGCTGCAGGTTTGGGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 ATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTGGAACCAGATGATAAAGGT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope - Centre National de Sequencage
BP 191006 EVRY cedex - France
Email: seqref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: flang@lifetech.com l
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO79DG08NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX361080 Homo sapiens PLACENTA COT 25-NORWALIZED Homo clone CS0DI079YN16 3-PRIME, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mrna"
/mol_type="mrna"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="CSDDIO/39VN16"
/tissue_type="placenta COT 25-NORMALIZED"
/clone_Tib="Homo sepiens placenta COT 25-NORMALIZED"
/note="Ist strand cDNa was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNa was
digested with Not I and cloned into the Not I and ECOR V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sites of the pCMVSPORT 6 vector. Library was normalized
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38.6; D. Pred. No. 28; 7; Mismatches
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AUTHORS
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ORGANISM
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                                                                                                                           DEFINITION
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Best Local S
Matches 89
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    ORGANISM
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                                                                                                                                                                                                                                                                                              372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252
                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                   LB01712a.d_SP6.1 Leishmania major Friedlin BAC Library Leishmania major genomic clone LB01712a, genomic survey sequence.
BH87860
BH87860.1 GI:22133383
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate; 13 row: F column: 02
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR PRimers
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales, Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea Unpublished (2003)
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OSUNEc13F02.f OSUNEc Oryza sativa (japonica cultivar-group)

Clone OSUNEc13F02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85721-0088, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Rod Wing
Leishmania major
Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                CCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACTGCGGC 425
                                                                                                                                                                                                                                                                                                                                    ATGCCGCCGGGTGTTCGACCGGATCGCGCACCCGACCTGCCGGCCTGGAACGCGCTGCT
                                                                                                                                                                                                                                                                                                                                                                            CTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGGGTCAAAAACCCCATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                       CGCCCTCGTTGTGGGCGCAGCGCCCTGGGCGCCATCGCGCTCACCACATTGCTGGTGAA 311
                                                                                                                                                                                                                                                      CTCCGCCTACGCGCGTCTTCGTGCCAGGGACGTGGCCTGCGCCACCTCTGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="OSJNEc"
/clone lib="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 6 hrs after innoculation with Rice Blast (C9240-1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEC13F02"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.1%;
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r-group) cDNA
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                                                 Homo sapiens (human)
M Homo sapiens
Eukarycta; Metazoa; Chordata; Craniata; Verteb:
Mammalia; Butheria; Primates; Catarrhini; Homin
1 (bases 1 to 1108)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDuA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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83; Conserv
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Other GSSs: LB01712a.d_T7.1
Other GSSs: LB01712a.t_T7.1
Contact: Myler PJ
Seattle Biomedical Research Institute
Seattle Biomedical Research WA 98109-1651,
                                                                                                                                                                                                                                                                                                           BX382084 Homo sapiens PLACENTA COT 25-NORMALIZED Homo CS0DI074YC24 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mylerpj@sbri.org
Seq primer: SP6
Class: BAC ends.
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Myler, P.J., Vogt, C., Munden, H., Robertson, L., Sisk, E.,
Fazelinia, G., Aggarwal, G., Nelson, S., Seyler, A., Worthey, E.,
Stuart, K. and Ragland, M.
Leishmania major Friedlin BAC End Sequences
                    Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                     BX382084.1 GI:30455015
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Fax: 206 284-0313
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Leishmania.
Email: segref@genoscope.cns.fr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trecreereaacriceeceacerarrerarecerirrea 339
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/note="Vector: pCG270; Site 1: HindIII; Genomic DNA from
Leishmania major Friedlin in agarose blocks was partially
digested with HindIII, size selected, and ligated with
HindIII-digested pCG270 vector DNA. 10368 clones were
picked and arrayed in 384- and 96-will plates. Library
construction and arraying was carried out by ResGen
Corporation and clones and filters are available from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Leishmania major"
/mol_type="genomic DNA"
/strain="Friedlin"
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1. .697
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/clone="LB01712a"
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                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
Web : www.genoscope.cns.fr
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EST 08-MAY-2003

sapiens cDNA

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                                                                                                                                                                                                                                     BGB45919 730 bp mRNA linear EST 29-MAY-2 [1024011F06.xl C. reinhardtil CC-1690, normalized, Lambda Zap II Chlamydomonas reinhardtil cDNA, mRNA sequence.

BGB45919 BGB45919.1 GI:14227103
BST. Chlamydomonas reinhardtil Chlamydomonas reinhardtil Chlamydomonas reinhardtil
Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermott, J.P., Sifflow, C., Stern, D. and Surzycki, R. Analyses of the Chlamydomonas reinhardti Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2 Unpublished (2000) Contact: Charles Hauser DCMB Dox 91000 COMB DOX 91000
                                                                                                                                                                       Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 730)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/db_xref="taxon:9606"
/clone="CSODI074YC24"
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Pred. No. 57;
5; Mismatches 189;
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Tel: 919 613 8159
Fax: 919 613 8177
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Contact: Robert Strausberg, Ph.D.

Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 1454)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NC 27708-1000
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/strain="CC-1690 wild type mt+ 21gr"
/strain="CC-1690 wild type mt+ 21gr"
/clone_lib="C. reinhardtii CC-1690, normalized,
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                                                                                                                                                                                                                                                                      Email: walbot@stanford.edu
Plate: 1008061 row: 27
                                                                                                                                                                                                                                                                                                                               Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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Location/Qualifiers
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/note="organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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/tlssue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
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/strain="FVB/N"
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/mol_type="mRNA"
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/mol type="genomic DNA"
/cultivar="mixed background
/db xref="taxon:4577"
/tlssue_type="leaf"
                                                                                                                               organism="Zea mays"
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Pred. No. 74;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 TTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCCTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397 ATCGACGAAGCCTACGCAGTCACTGC 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                                                                                                                        Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS016BR 1201 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BAC(library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL106545.1 GI:5622456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rredeceda erecidence redecede recentar de recenta de consecuencia de la recenta de la 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 1201)
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//lab_nost="DH10B"
//clone_lib="1008 - RescueMu Grid I"
//clone_lib="1008 - RescueMu Grid I"
//clone_lib="1008 - RescueMu (engineered from note=""Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BgIII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmdb.isstate.edu and follow the links for 'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BgIII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic survey sequence.
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db xref="gaxon:7227"
/clone="BACN15K14"
                                                                                                                                                                                                                                      Location/Qualifiers
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Pred. No. 55;
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clone_lib="DrosBAC"

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В 8

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RESULT 15
BE013856/c
LOCUS
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AUTHORS
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ORGANISM
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ACCESSION
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                                                                                   FEATURES
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Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 TTGGTCTCTTGGTTATTCAATACGGCTACGAATGGTGGGCAGC-CCCACTGTTTTCCGGC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (Bess 1 to 539)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J., Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush,J. and Keele,J.W.
Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
                                                                                                PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
FORWARD: GTTTTCCCAGTCACGACG
BACKWARD: GTTTTCCCAGTCACACG
Plate: 52 row: G column: 21
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                      Contact: Smith TPL USDA, ARS, US Meat Animal Research Center DSDA, ARS, US Meat Animal Research Center DSDA 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366

Tel: 402 762 4366

Fax: 402 762 4390

Email: smithpemail.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE013856 539 bp mRNA linear
125354 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BE013856
BE013856.1 GI:8274843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YIGGGKBCCRGGTIMVSCSSSGGSSSCCGKTVGSCSSSSCCSSGSCCSCBCTCGSSSSSS 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVVMVSYCCCCMMAGGMACCHICATKGCCMGDGASCCGDSVSSSGGSCCVRSSSVGRMYH 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTCCCMAWCMCMCMAAMMMCCCTYCKMAGTANCTCWMAMMMMCSGGSCAAMMVVVVVMV 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCATTCCCGCTGCATGTGGAAAAACCCCATTGCCCGTTTCTATTCGGTTTTCGCGC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CBCCCCSCKCCGBSGSTSKSSTGKGTBGKGSSSKGGGGGGKSSBSSSSBTSBBSBSNTSSS 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITIBBSSSTTSSTTSBSGSBBTTBBSSBSTSTSSBTBYTTSTTBTKSSSBTSTSSSKB 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 131; Mismatches 153; Indels
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/note="end : T7"
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.9%; Score 36.8;
20.4%; Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 29;
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'tissue_type="pooled"

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Query Match
Best Local S
Matches 75
325
                                331
                                                                  385 CCGGCCCAGGGAAGCAGCCACCCCCACCCTCCTGCAGACCCAGGGAGCGGCAGTCAAG 326
                                                                                                                                         445
                                                                                                                                                                     211 TCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCGCA 270
                                                                                                     271 GCGCCCCTGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTTCCGCCACGTATTCTAT 330
                                                                                                                                                                                                               75;
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                          GCGTTTTCATTCCCGCTGC 349
GrenciecaAGCCCGCTGC 307
                                                                                                                                       TCTGGCTGGGCTTGCCCAGGCGAGCGTGAGGGGTGTGTGAGGGGCTGGTACAGAGATCA
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
/clone lib="MARC IPIG"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
/ibrary made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                                                                                                                                                                                            4.9%;
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Pred. No. 67;
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Search completed: April 17, 2004, 20:01:43 Job time: 2440.38 secs

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Aag93154 C glutami
Abg66261 Bifidobac
Abm69066 Photorhab
Abp57756 E coli L
Ada33529 Acinetoba
Adc95293 E. faeciu
Abu00481 S. pneumo
Abp81300 Streptoco
Abb54959 Lactococc
Abb47959 Listearia
Abp30530 Streptoco
Abp28562 Streptoco
Abp40309 Straphyloc
Aag81587 S. epider
Adb08660 Alloiococ
Adb08660 Alloiococ
Adm72815 Staphyloc
Adm34737 Acinetoba
Aau64076 Propionib
Abm60595 Propionib
Abm60595 Bridobac
Abb55268 Lactococcc
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ALIGNMENTS

RESULT 1 AAG90035 ID AAG9 16-DEC-1999; 07-APR-2000; 03-AUG-2000; Coryneform bacterium; a organic acid synthesis. C glutamicum protein fragment AAG90035; AAG90035 standard; protein; 251 18-DEC-2000; 20-JUN-2001. EP1108790-A2 Corynebacterium glutamicum 26-SEP-2001 99JP-00377484. \2000JP-00159162. 2000JP-00280988. 2000EP-00127688. (first entry) amino acid synthesis; vitamin; saccharide; SEQ ID NO: 3789. ₿

(КУОМ) КУОМА НАККО КОБУО КК.

Nakagawa Tateishi 'n, Mizoguchi H, Ando Senoh A, Ikeda M, S, Hayashi M, Ozaki A; Ochiai K, Yokoi H;

WPI; 2001-376931/40. N-PSDB; AAH65254.

Novel polynuclectides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene

Claim 17; SEQ ID NO 3789; 246pp + Sequence Listing; English

The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteriam are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the

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Matches 251
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This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) polypeptides; (ii) encodes a polypeptide at least 70% identical with (3) or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB86247
                                                                                                                                                Claim la;
                                                                                                                                                                                                                           New export
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2001.
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                                                                                                                                                                                               New export genes from coryneform bacteria, useful for fermentative production of branched-chain amino acids
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DB; AAH21109, AAH21110.
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orm bacterium; leucine;
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FORSCHUNGSZENTRUM JUELICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKGLEFALCSLFVTLTLDSCRTKKQIPSLLLAGLSFTIALVVIPGQALFAALLIFLGLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IKGLEFALCSLFVTLTLDSCRTKKQIPSLLLAGLSFTIALVVIPGQALFAALLIFLGLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPIARFYSVFALIDEAYAVTAARPAGWSAWRLISMQIAFHSYWVFGGLTGVAIAELIPFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPLGAIALTTLLVNFRHVFYAFSFPLHVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRYFFLGKAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRYFFLGKAAK
                                                                                                                                                   Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99DE-01051708.
                                                                                                                                                   15-16; 23pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glutamicum
                                                                                                                                                                                                                                                                                                                                             Eggeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                      German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 AA
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Pred. No. 3.3e-137;
                                                                                                                                                                                                                                                                                                                                                Sahm H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brnE; branched-chain amino acid;
isoleucine; valine; medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 GMBH.
                                                                                                                                                                                                                                                                                                                                                Pfefferle
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                                                                                                                                                                                                                           increasing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
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                                               CC protein derived from (i)-(iii). The invention also describes (a) CC protein derived from sequences of 753 bg (2) or 324 bg (4); (b) CC coryneform microorganisms, especially Corynebacterium, transformed with CC one or more (I), where these are replicative DNA; (c) production of Dranched-chain L-aa by fermentation of coryneform bacteria in which the CC brnB and/or brnF genes (or equivalent sequences) are amplified, CC especially overexpressed; and (d) method for isolating the brnB and/or brnF genes. (I) is used for transformation of coryneform bacteria being CC used for fermentative production of branched-chain amino acids, specifically elucine, isolaucine and valine, which are useful in medicine CC and animal nutrition. (I) can also be used as source of primers and CC probes for isolation of related sequences. Transformation with (I) CC increases yield of branched-chain amino acids. This sequence represents CC the Corynebacterium glutamicum ATCC 14752 brnF protein described in the CCC method of the invention
Sequence 251 AA;
                                                                                                                                                                                                                              in medicine
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Length

Ś 밁 8 밁 Ş Ś 밁 Ş 밁 跊 Query Match Best Local Sim Matches 250; 121 241 241 181 181 121 61 61 ш Similarity 99.6 50; Conservative GYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPLGAIALTTLLVNFRHVFYAFSFPLHVVK NPIARFYSVFALIDEAYAVTAARPAGWSAWRLISMQIAFHSYWVFGGLTGVAIAELIPFE QKTQBIHSSLEVSPSKAALEPDDKGYRRYEIAQGLKTSLAAGLGMYPIGIAFGLLVIQY NPIARFYSVFALIDEAYAVTAARPAGWSAWRLISMQIAFHSYWVFGGLTGVAIAELIPFE VQXTQEIHSSLEVSPSKAALEPDDXGYRRYEIAQGLKTSLAAGLGMYPIGIAFGLLVIQY IRYFFLGKAAK IRYFFLGKAAK 251 IKGLEFALCSLFVTLTLDSCRTKKQIPSLLLAGLSFTIALVVIPGQALFAALLIFLGLLT IKGLEFALCSLFVTLTLDSCRTKKQIPSLLLAGLSFTIALVVIPGQALFAALLIFLGLLT GYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPLGAIALTTLLVNFRHVFYAFSFPLHVVK 99.7%; 99.6%; 251 ۲. Score 1265; DB 4; Pred. No. 9.4e-137; 1; Mismatches 0; 0 Gaps 240 60 240 120 120 180 180

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RESULT 3
AAG93154
ID AAGS
16-DEC-1999;
07-APR-2000;
03-AUG-2000;
      Nakagawa
Tateishi
                                                                                                                       Coryneform bacterium; amino organic acid synthesis.
                                                                                                                                           C glutamicum
                                                                                                                                                          26-SEP-2001
                                                                                                                                                                        AAG93154;
                                                                                                                                                                                    AAG93154 standard; protein;
                                                                  18-DEC-2000; 2000EP-00127688
                                                                                20-JUN-2001.
                                                                                                           Corynebacterium
                         (KYOW ) KYOWA HAKKO KOGYO
      zία
                                       99JP-00377484.
2000JP-00159162.
2000JP-00280988.
     Mizoguchi
Senoh A,
                                                                                                                                            protein
                                                                                                                                                          (first
                                                                                                           glutamicum.
                                                                                                                                                          entry)
                                                                                                                                            fragment
     . H, Ando
Ikeda M,
                           겆
                                                                                                                                                                                      237
                                                                                                                               acid synthesis; vitamin;
                                                                                                                                             SEQ
                                                                                                                                                                                      ይ
      S, Hayashi
Ozaki A;
                                                                                                                                             ID NO:
                                                                                                                                              6908
             3
              Ochiai
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Yokoi

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saccharide;

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ARBSULT 4
ARBSCATCH
ARBSCA
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Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; SEQ ID NO 6908; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonalla; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bacteria; rotavirus; food composition; pharmaceutical composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP66261 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 237 AA;
      WPI; 2002-668397/72
                                                                                                                            30-JAN-2001; 2001EP-00102050
                                                                                                                                                                                         30-JAN-2001; 2001EP-00102050.
                                                                                                                                                                                                                                                                                                                                                                                      Bifidobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 EIAQGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALV-VG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AWRLISMQIAFHSYMVFGGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDSCRTKKQIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLAGISFTIALVVIPGOALFAALLIFLGLLTIRYFF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTRVLTVQILCQALWVIPGIIGALVGQVLPDDLKGMDFALTALFVVLAWEAFKNNKDYSL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGPFSA-AVAGFMVNFRHIFYGLTFPRHRIKSGAGRAYSTYALTDESYAIVSARPPGDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAPLGAIALTTLLVNFRHVFYAFSFPLHVVKNPIARFYSVFALIDEAYAVTAARPAG-WS
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                                                                PROD NESTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                longum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.8%;
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Pred. No. 1.5e-40;
6; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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Novel polynucleotide comprising Bifidobacterium genome sequence useful a probe or primer for detecting and/or identifying Bifidobacterium long in a biological sample.
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Claim 3; SEQ ID NO 1005; 80pp; English

CC sequence of a Bilidobacterium genome selected from the nucleotide
CC sequences given in ABQB1842 and ABQB1843, or a sequence exhibiting at
CC least 90% identity or which hybridises with the sequence given in
CC ABQB1842 and ABQB1843. Also described is a polynucleotide (II) encoding a
CC in ABP65258 to ABP66354 ligated in frame to a polynucleotide encoding a
CC activities, and can be used as an inhibitor of Salmonella. (I) (which is
CC aprobe) is useful for the detection and/or identification of
CC Bifidobacterium longum in a biological sample. A carrier containing the
CC lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) can be
CC used for preventing and/or treating diarrhoes brought about by pathogenic
CC bacteria and/or rotavirus. The carrier is a food composition selected
CC products, ice-creams, fermented cereal based products, milk based
CC supplement, wet oral supplement, dry tube feeding or wet tube feeding.
CC (I) is useful in DNA arrays or chips to carry out analysis of the
CC expression of the Bifidobacterium gene. ABQB1844 to ABQB1850 represent
CC Ensting from the present invention but not mentioned further within the
CC specification. N.B. The sequence data for this patent is not represented
CC in the printed specification but is based on sequence information
CC supplied by the European Patent Office The present invention describes a polynucleotide (I)

Sequence 338 AA;

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Matches
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270
                                                                                                                                                      103
                                                                                       152 LISMQIAFHSYWVFGGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDSCRTKKQIPSL-L
                                                                                                                                                                                    99
                                                                                                                                                                                                                44 LGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGA-APLGAIALTTLL
                                                                                                                                                                                                                                                64;
                                                                                                                                                                                                                                                               Similarity
                             LAGLSFTIALVVIPG-----QALFAALLIFLGL
                                                                                                                       VNARHLFYGLSM-----LGKFKGLGWKRPYLIFGMCDETFAINSTAKIPAGIDRGWF
                                                                                                                                                      VNFRHVFYAFSFPLHVVKNPIARF------YSVFALIDEAYAV--TAARPAGWS-AWR
VIGVLTSLACLLIFGANDFMIPSMIAMLILFVAL
                                                         YFWVTLCNOLYWVTGATLGGLIGAHLPFNTDGLDFVLTALFLVIFLDQWLDGKHRERLSA
                                                                                                                                                                                    LGFLFLGASYGILMGTKGFSFVWPMCMSAFIFAGSMEFVTVNLLLSAFNPLAGF-LLALM
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                             16.9%;
                                                                                                                                                                                                                                                37;
                                                                                                                                                                                                                                              Score 214; DB 5; I
Pred. No. 1.1e-15;
Pred. No. 1.8 5;
303
                                                                                                                                                                                                                                                                            Length 338
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                    157
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ARMSOLT 5
ARMSOL 5
ARMSOL ARMS
XX ARMS
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B

Photorhabdus luminescens protein sequence #2163

20-NOV-2003

(first entry)

Antibacterial; fungicide; insecticide; polymorphism; genetic detection; food; gene expression; plant; animal; microorganiantibiotic; biopesticide; virulence factor; disease model; plantibiotic; whooping

Photorhabdus luminescens

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Buchrieser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. luminescens. Cells transformed to express the genes are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                      recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic sequence of Photorhabdus luminescens and useful e.g. as therapeutic antimicrobials and agr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-148459/14
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                                                                                                                                                                                                                                                                                                                                                                                                           261
                                                                  AIEAAMIFMLPALFLSFLLASCRKONSYCVATALTGALLGITFFSIPVAILAGIVGGCIA
                                                                                                                                                                  ---FALIDEAYAVTAAR----PAGWSAWRLISMQIAFHSYW----VFGGLTGVAIAELIP
                                                                                                                                                                                                    FSCIIYAGASQFVITALLSAGTSLWISALTIMAMDVRHILYGPSL-RHRIKDKLTEKKTV
                                                                                                                                                                                                                                   FSGLIFAGSTEMLVIALVVGAAPLGAIALTTLLVNFRHVFYAFSFPLHVVKNPIARFYSV 129
                                                                                                                                                                                                                                                                     SMPVSDTSSPLTS----KKSSFTEGIIDSLPIVIGYIPVAFAFGLNAVKLGFNPMEAIF
                                                                                                                                                                                                                                                                                                      SLEVSPSKAALEPDDKGYRRYEIAOGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPL
                                                                                                                                 IWAFGITDEVFAAATAKLIKNHRSWSENWYVAIAICSWLAWGAGTAAGAFLGNGYLESYP
                                                                                                 FEIKGLEFALCSLEVTLTLDSCRTKKO-----IPSLLLAGLSFTIALVVIPG--QALFA
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                                                                                                                                                                                                                                                                                                                                                        15.6%;
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                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                        Score 197.5; DB 6
Pred. No. 6.2e-14;
4; Mismatches 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frangeul L,
                                                                                                                                                                                                                                                                                                                                                                       DB 6;
                                                                                                                                                                                                                                                                                                                                        110;
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                                                                                                                                                                                                                                                                                                                                                                       Length
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RESULT 6 ABP57756

RESULT 7
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ADA35238 standard; protein;

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Matches 68
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26-FEB-2001;
28-JUN-2001;
28-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel L-amino acid producing bacterium of genus Escherichia, modified to enhance L-amino acid production by enhancing the activities of a protein. The novel bacterium is useful for producing L-amino acid e.g. L-Thr, L-Val, L-Pro, L-Leu, L-Met and L-Arg, by cultivating the bacterium in a culture medium and collecting L-amino acid to be produced and accumulated from the culture medium. The present sequence represents a protein of the invention which causes increased L-amino acid production in E. coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel L-amino acid producing Escherichia bacterium, is modified enhance L-amino acid production by enhancing the activities of propable of making bacterium to have enhanced resistance to L-amino acid production by enhanced resistance to L-amino acid production by the second control of the second control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2002; 2002EP-00003335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 23; 33pp; English.
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195
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                                                                                                                                                                                                                                                         94 GAIALTTLLVNFRHVFYAFSFPLHVV----KNPIARFYSVFALIDEAYAVTAAR----PA
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                                                                                                                                                                                                                                                                                                                                                                  34 QGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPL
                                                                                                                                                                                                                                                                                                                                                                                                                             68;
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                                                                                                      RWSENWMIGIAFSSWSSWVFGTVIGAFSGSGLLQGYPAVEAALGFMLPALFMSFLLASFQ
                                                                                                                                                   GWSAWRLISMQIAFHSYWVF----GGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDSCR
                                                                                                                                                                                                            WIAALTVMAMDVRHVLYGPSLRSRIIQRLQKSKTALW--AFGLTDEVFAAATAKLVRNNR
                                                                                                                                                                                                                                                                                                                  EGCKDSLPIVISYIPVAFAFGLNATRLGFSPLESVFFSCIIYAGASQFVITAMLAAGSSL
                                                   TKKQIPSLLLAGLSFTIALV-VIPGQALFA---ALL--IFLGLLT--IRYFFLG
                                                                                                                                                                                                                                                                                                                                                                                                                  15.5%;
nilarity 29.1%;
Conservative 41
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; 2001RU-00104998.
; 2001RU-00104999.
; 2001RU-00117632.
; 2001RU-00117633.
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-SICVTAALVGALAGVTLFSIPVAILAGIVCGCLTALIQAFWQG
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                                                                                                                                                                                                                                                                                                                                                                                                                             41;
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Pred. No. 6.5e-14;
1; Mismatches 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as respents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acinetobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccines,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     baumannii
                                                                           ADA33199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acinetobacter baumanii proteins and nucleic acids, useful as reagents diagnosing a bacterial disease, as components of antibacterial cines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003-576092/54.
)B; ADA31112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tobacter baumannii; bacterial disease; biocontrol agent.
                                                                                                                                                                          212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID
                                                                                                                                                                                                                                                                                                                              WLTALTVIALDIRHVLYGPALYNLIPTKLNLKKTAV----WAWGLTDEVFASGMIQLSQR
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                                                                                                                                                                                                                                                                                       PAGWSAWRLISMQIAFHSYW----VFGGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDS
                                                                              standard;
                                                                                                                                                                          FERKHS---
                                                                                                                                                                                                             CRIKKQIPSLILLAGUSETIALVVIPGQALFAALLIFUGUUT-----IRYFFU 246
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                                                                                                                                                                        -LVVAVSLVVSALACYWINLSAA--İFIĞILSGILAGLFKYYVL
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                                                                           protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 190; DB o; Pred. No. 4.6e-13;
                                                                              263
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20-NOV-2003 ADA33199;

(first entry)

01-JAN-2004 ADC95293;

(first entry)

faecium

protein

sequence

SEQ

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ADC95293 standard;

protein;

255

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                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A. baumannii protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acinetobacter baumannii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acinetobacter baumannii protein #360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-576092/54.
N-PSDB; ADA29073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6562958-B1
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biocontrol
                                                                                     172
                                                                                                                                                                      113
                                                                                                                                                                                                    100 TLLVNFRHVFYAFSFPLHVVKNPIARFYSV-FALIDEAYAVTAARPAGWSAWRLISMQIA
          232
                                                                                                                           159
                                                                                                                                                                                                                                                 53
                                                                                                                                                                                                                                                                                       40
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                                                                                                                                                                                                                                               LPLSISVIPWAILAGSMAVHAGLSFYKALAMSGIVFAGAAQLVSLSMVMEGASLLTIYVT
                                                                                                                                                                                                                                                                                     LAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPLGAIALT
                                                                                                                                                                                                                                                                                                                                                                                                               263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4486; 328pp; English.
                                                                                                                                                                  IFFLTAQHFIYALTLRNDISILPLSKRLTLGFLLTDELFAVSVPNEKKHPQY-LFGAGLC
VLKFFHİEGAILISGLLGMFIAVI
                                            TIALVVIPGQALFAALL-IFLGLL
                                                                                     FYLFWVVFSLVGILLATALPNLLNYHLDFSIIAIFVAMIVPMCKGKPVMAGILMTCVSGF
                                                                                                                         FHSYWVFGGLTGVAIAELIPFEIK-GLEFALCSLFVTLTLDSCRTKKQIPSLLLAGLS-F
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         baumannii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0088701P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agent.
                                                                                                                                                                                                                                                                                                                                             14.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacterial disease;
                                                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                                                                                                                                                                                Score 189.5; DB 6;
Pred. No. 5.2e-13;
4; Mismatches 96;
                                                 239
            255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                             263;
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                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid derived from CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having CD enterococcus faecium polypeptide having CD enterococcus faecium polypeptide having CD enterococcus faecium polypeptide having CD enterococcus faecium polypeptide having CD enterococcus faecium polypeptide having CD enterococcus faecium enterococcus faecium polypeptide having CD esquential mucleotides chosen from any of the nucleic acids, its CD enterococcus faecium polyperion in the enterococcus faecium polyperion any of the nucleic acid operably linked to CD examscription regulatory element, a cell comprising the vector and a CD single-stranded probe comprising the nucleic acid. The nucleic acids are CD enterococcus faecium bacterial infection (e.g. urinary tract CD enterococcus faecium bacterial infection (e.g. urinary tract CD enterococcus faecium production and antagonists. The CD enterococcus faecium production of Candida albicans CD enterococcus faecium infections. The present sequence represents containing the nucleic acid are useful for preventing or CD enterococcus faecium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NC 4920; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid derived from Enterococcus faecium encoding Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADC91639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-1997;
14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-799836/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6583275-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    one if the disclosed E. faecium proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENO-) GENOME THERAPEUTICS CORP.
                                                                                   184
                                          185
                                                                                                                                                                  135 EAYAVTAARPAGWSAWRLISMQIAFH------SY--WVFGGLTGVAIAELIPFEIK-G
                                                                                                                                                                                                          71
                                                                                                                                                                                                                                                 76
                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                                16 SKAALEPDOKGYRRYEIAQGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIF
                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                                                                               Similarity
--LGLLTIRYFF 245
                        LDFAIVAMFIGLLYLQVISDRNTSKRL-QLILIGLTLILVYVGLIFIFSNLVIVVVTLIG 243
                                                                                                                                                                                                          AGSAQFITVSMLASHSPLLSIVFSTFLVNSRMILMSMTIAPYFKKNRLLQNLLIGTLLTD
                                                                                                                                                                                                                                               AGSTEMLVIALVVGAAPLGALALTTLLVNFRHVFYAFSFELHVVKNPIARFYSVFALI-D
                                                                                                                                                                                                                                                                                            AKGVLLLDEK----LDIKTAIKDTLPTVFGYIGIGLAFGIVGKAAGFHPLVVTLMSLLVY
                                                                                                                       ESFAL-----GMNKLNYTGQKLNFRWMNTANWISYLTWVGSSLVGALLGNFITDPKKFG
                                                                              LEFALCSLFVTL----TLDSCRTKKQIPSLLLAGLSFT---IALVVIPGQALFAALLIF- 235
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0051571P.
98US-0085598P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9805-00107532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bush D;
                                                                                                                                                                                                                                                                                                                                                                        14.6%; Score 185.5; DB 7;
25.0%; Pred. No. 1.4e-12;
tive 51; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                             Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 255;
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RESULT 10
ABU00481
ID ABU00
CC identity to any of the 2469 amino acid sequences, identify to any of the 2469 amino acid sequences, identified in the compressed from 2469 of 2489 identified DNA coding regions from the CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as CC treating a patient by administering the protein, DNA or antibody (in a CC composition), a kit comprising first and second primers, which are the cC nucleic acid cited above or fragments between nucleotides 8-100 of a CC sequence contained within a Streptococcus nucleotides 8-100 of a CC sequence contained within a Streptococcus nucleotides 8-100 of a CC sequence contained within a Streptococcus nucleotides 8-100 of a CC sequence contained within a Streptococcus nucleot acid sequence, where CC the first primer is substantially complementary to the target sequence of the target sequence and where the parts of the primers having substantial complementary to the target sequence to be amplified, assay comprising contacting a test compound with the CC substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound with the CC substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound with the CC sucid molecules, antibody and compositions are useful as medicaments for CC treating or preventing a disease or infection the proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for CC media or ear infection. They are also useful in developing vaccines, otitis medica or ear infection. They are also useful in developing vaccines, otitis medication, but was obtained in electronic format directly from WIPO Ca tfp.wipo.int/pub/published_pct_sequences. (Updated on 23-0cT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;

    pneumoniae type 4 strain protein from coding region

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-2003
11-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU00481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 96; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ear infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABX05760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-2001; 2001GB-00007658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2002; 2002WO-IB002163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200277021-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae; type 4 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU00481 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-040579/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHIRON SPA.
INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C;
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ABPSULT 11
ABPS1300
ID ABPS1
XX ABPS1
XX ABPS1
XX ABPS1
XX O4-MA
XX Strep
XX Strep
XX Strep
XX W0200
XX W12-AE
XX H2-AE
XX H2-AE
XX H2-AE
XX 16-AE
PR 18-AE

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Best Local S
Matches 63
                                                                                                                                      The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) of a Streptococcus pneumoniae genomic sequence, a fragment or degenerate variant of the polynucleotide or a nucleic acid sequence 95% identical to one of the polynucleotides. The S. pneumoniae polynucleotides and encoded polypeptides (ABPB1299-ABPB1574) are useful for treating or preventing S. pneumoniae infections or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. These are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pr
diagnosis; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                               New Streptococcus pneumoniae polynucleotides, useful for treating operenting S. pneumoniae infections, or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zagursky
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18-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP81300
                                                                                 are induced or exacerbated by S. pneumoniae. These are also useful for detecting S. pneumoniae in a biological sample or diagnosing S. pneumoniae infection in a subject. The polynucleotides have antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-APR-2002; 2002WO-US011524
                                                                                                                                                                                                                                                                                                                                                Claim 42; Page 349-350; 1091pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMCY ) AMERICAN CYANAMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2003-093010/08.
DB; ABZ42148.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         μ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y RJ,
JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKKQIP-----SLLLAGLSFTIALVVIPGQ--ALFAALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NPMWMHGNNLNSYVA----WFVGTVVGTALGGLLPNPEIFGLDFALVGMFIGIFASQFQI 167
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Pred. No. 9.7
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Sequence

218

Query Match 13.8%; Best Local Similarity 25.5%; Matches 61; Conservative (

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Best Local S
Matches 63
                                                 The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at
                                                                                                                                                                                                                 Claim 6; SEQ ID NO 1661; 2504pp; French
                                                                                                                                                                                                                                                                                                                                                                           11-APR-2000; 2000FR-00004630
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16-MAY-2002
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Sequence 235
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standardise OS field)
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(first entry)
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6; Mismatches 8:
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RESULT 13
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The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, an for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listeria monocytogenes.
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ons, and related
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Cossart P;
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Amend A;
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New Streptococcus protein for the treatment or disease caused by Streptococcus bacteria, such detecting a compound that binds to the protein.

prevention of as meningitis,

infection, and for

ő

Page 4153;

4525pp;

English.

The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in

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RESULT 14
ABB30530

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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DB; ABN71161.
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
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24-NOV-2000; 2000GB-00028727
07-MAR-2001; 2001GB-00005640
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N-PSDB; ABN69193.
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Tettelin H;
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CC (Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (C) (Streptococcus/GAS (C) (Streptococcus/GAS (C) (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory cativity. (I), nucleic acids encoding (I), ABN66044-ABN71826 and attibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

CC Nucleic acids encoding (I) are used to detect Streptococcus in a combosition comprising (I) or a nucleic acid encoding (I), may be used to determine whether a compound binds to CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to a vaccine or diagnostic composition. The disease caused by CC streptococcus that is prevented or treated may be meningitis. Nucleic caid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity and may be represented the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the pro
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                                                                                             Streptococcus proteins
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Query Match Best Local S Matches 58 169 190 110 135 5 8 84 IALVVGAAPLGAIALTTLLVNFRHVFYAFSFPLHV-----VKNPIARFYSVFALI-D 24 DKGYRRYEIAQGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLV w Similarity AMFIGLEV----FQLEGMLSDGKRLVVYVLASVGLSYFLLATFLSGALSV SLEVTLTLDSCRTKKQIPSLLLAGLSETIALVVIPGQALFAALLIFLGLLTI EAYAVTAARPAGWS----AWRLISMQIAFHSYWVFGGLTGVAIAELIPF-EIKGLEFALC 189 CALLLAKADIMTITMTVFLVNLKNMLMS----LHATTIFKSAHLMNQLA----IGTLITD ESYGVLLGEALHHKVVSPSW-MHGNNVMSYLTWVISTIIGTLLGSTIPNPEMFGLDFALV Conservative 13.2%; 43; Score 167; DB 5; Length 231; Pred. No. 1.7e-10; 3; Mismatches 97; Indels 34; 241 214 Gaps 168 109 134 57

Sequence 231 AA;

Search completed: April 16, Job time : 73.6156 secs 2004, 06:53:11 Ś 밁 Ś 밁 Ś B Ś

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Sequence 6024, Ap
Sequence 6789, Ap
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ALIGNMENTS

Sequence 3, Application US/09471803A Patent No. 661345 Patent No. 661345 Patent No. 661345 APPLICANT: KENNERKECHT, NICOLE APPLICANT: SAHM, HERMANN APPLICANT: SAHM, HERMANN INTITE OF INVENTION: NUCLECTIDE SEQUENCE CODING FOR THE EXPORT OF TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF FILE REFERENCE: 21133/26496/WAS CURRENT APPLICATION NUMBER: US/09/471,803A CURRENT APPLICATION NUMBER: US/09/471,803A CURRENT APPLICATION NUMBER: DE 199 51 708.8 PRIOR APPLICATION NUMBER: DE 199 51 708.8 PRIOR FILING DATE: 1999-10-27 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3 LENGTH: 251 ; TYPE: PRT ; ORGANISM: Corynebacterium glutamicum ; FEATURE: ; OTHER INFORMATION: ATCC14752 US-09-471-803A-3 THE

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Score 1269; DB 4; Pred. No. 2.6e-138; ; Mismatches 0;

Length Indels

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US-09-489-039A-8478
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Matches 62
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Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 6525
LENGTH: 266
TYPE: DEF
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APPLICANT: Gary Bro
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAWRLI---SMOIAFHSYWVFGGLTGVAIAELIP-FEIKGLEFALCSLFVTLTLDSCRTK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLGVIIFTTLIINLRHVLYSASISGTVRE---ASFFKKCFMSYALTDEVYATTVKEMEGN
                                    GAIALTTLLVNFRHVFYA-----FSFPLHVVKNPIARFYSVFALIDEAYA----VTAAR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTVAAVVAAVS-GVLLVVLPYSLGIVVASVLGVLAGL
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                                                                   CGAKDSQAIVLTYLPVSFAFGVSASQFGFTPWEAFFLSCSMYAGASQFLVVALIASGSSI 95
                                                                                                                QGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPL 93
  WLTALTVIALDIRHVLYGPALYNLIPTKLNLKKTAV----WAWGLTDEVFASGMIQLSOR 151
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                                                                                                                                                       Conservative
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                                                                                                                                                     43; Mismatches
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Pred. No. 2.4e-17;
                                                                                                                                                                        Score 190;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 101;
                                                                                                                                                                        DB 4; Length 266; .1e-13;
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                                                                                                                                                       Indels
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RESULT 4
US-09-328-352-4486
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US-09-107-532A-4920
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SEQ ID NO 4486
LENGTH: 263
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Sequence 4920, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
APPLICANT: INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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Local Similarity 24.0%; Pred. No. 1.3e-13;
Les 49; Conservative 54; Mismatches 96
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                      ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 VLKFFHIEGAILISGLLGMFIAVI 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 TIALVVIPGQALFAALL-IFLGLL 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 LPLSISVIPWAILAGSMAVHAGLSFYKALAMSGIVEAGAAQLVSLSMVMEGASLLTIYVT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 TAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPLGAIALT 99
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                                                                                                    COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                   STATE: Massachusetts
                                                                                                                                                    MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                            STREET: 100 Beaver Street
                                                                                  SOFTWARE: ASCI
                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                          CITY: Waltham
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AND AMINO ACID SEQUENCES RELATING
FAECIUM FOR DIAGNOSTICS AND THERAF
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                                                                                                                                                                                                                                    Sequence 10187, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: ENEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION UNMEER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR #ILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10187
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Best Local
   Query Match
Best Local :
                                                                                                      ORGANISM: Klebsiella
-09-489-039A-10187
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Local Similarity
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FILING DATE: 14 MAY 19
APPLICATION NUMBER: 60
FILING DATE: July 2, 1
ATTORNEY/AGENT INFORMATION:
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LOCATION: (B) LOCATION 1...255
SEQUENCE DESCRIPTION: SEQ ID NO: 4920:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489 REFERENCE/DOCKET NUMBER: GTC-0: TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
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HYPOTHETICAL: YES
ORIGINAL SOURCE:
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63; Conserv
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   14.3%;
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       Score 181;
Pred. No. 1
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       DB 4;
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                                      Length 251;
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GENERAL INFORMATION:

APPLICANT: Gary Breton et. al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709-2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27

KLEBSIELLA

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RESULT 8
US-09-489-039A-12218
US-09-489-039A-12218
Sequence 12218, Application US/09489039A
Fatent No. 6610836
Fatent No. 6610836
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US-09-252-991A-27947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                     204
                                                                                                                                                                                                                                              145 AGWSAWRLISMQIAFHSYWVFGGLTGVAIAELIP-FEIKGLEFALCSLFVTLTLDSCRTK 203
                                                                                                                                                                                                                                                                                          177
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                                                                                                                                 293 -NVPTLVCVATSLFCSVLFSHWQ--WSSALVLAGL 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 VGEGVKDSLPIVISYLPVAFAFGLNATRIGFTPLESLFFSCIIYAGASQFVITAMLAAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 IAQGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGAA 91
                                                                                                                                                                                                                                                                                                                                                                                                           29 RYEIAOGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLWVAALTVMAMDVRHVLYGPSLRSRIRSALDKKKTALW--AFGLTDEVFAAATARLVRD 138
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                                                                                                                                                                                                       RNFNRWYALGVGLTFYIAWNLFTLAGILLGRSIPGLEHLGLDFSIAATFIALVAPLVR--
                                                                                                                                                                                                                                                                                                                                                                   RQAFLRGAVAILPLSLAVAPWGLLAGSMAIBANLTPAEGQGLSAIVFÄGAAQLVAIGMLK 176
                                                                                                                                                                   KQIPSILLAGLSFTIALVVIPGQALFAALLIFLGL 238
                                                                                                                                                                                                                                                                                          GGAGFFSIIFTTLLLTSQHLLYGMS--LRPVLSPLPGRWRIGLGFLLTDEFFALASQHDR
                                                                                                                                                                                                                                                                                                                              GAAPLGALALTILLVNFRHVFYAFSFFLHVVKNPIARFYSV---FALIDEAYAVTAARP- 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 175; DB 4;
; Pred. No. 8.9e-12;
47; Mismatches 104
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; TYPE: PRT; ORGANISM: Klebsiella US-09-489-039A-12218
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US-09-134-001C-5154
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PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12218
LENGTH: 288
                                                                                                                                                                                                                                                                                                                                                                                                                   PATENT NO. 6380370

GENERAL INFORMATION:
APPLICANT: LYMN DOUGETCE-Stamm et al
APPLICANT: LYMN DOUGETCE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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Best Local S
Matches 57
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 5154
LENGTH: 242
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57; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAASGAALALAAVPFVPTGLPVLLSLFGLLS
                                                               KGEKINDRW-----LHGLNITAYLEWTVSCVIGAIFGEYISNPDALGLDFAITAMFIFLCI
                                                                                                                                     SAIVLITLIVNSR-----MPLLSMTLAPNYKQYGFWNRVGLGTLLTDETFGV-AITPYV 132
                                                                                                                                                                    GAIALTTILVNFRHVFYAFSFPLHVVKNPIARFYSVF-----ALIDEAYAVTAARP-- 144
                                                                                                                                                                                                     QGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPL 93
 SOFEGIKKSRLRIYIVLIVCVIVMULLSSILPSYVAILI--AAIVAALL
                                  DSCRTKKQ-----IPSLLLAGLSFTIALVVIPGQALFAALL 233
                                                                                                   -----AGWSAWRLISMQIAFHSYWVFGGLTGVAIAELIPF-EIKGLEFALCSLFVTLTL 197
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nilarity 27.5%;
Conservative 41
                                                                                                                                                                                                                                                                      12.7%; Score 161.5; DB ilarity 24.8%; Pred. No. 2e-10; Conservative 40; Mismatches
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Pred. No. 1.8e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                        DB 4;
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                                                                                                                                                                                                                                                                                                        Length 242;
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                                                                                                                                                                                                                                                                           43;
     236
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RESULT 10
US-09-328-352-6024
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US-09-134-000C-6789
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TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6024
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6024
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GENERAL INFORMATION:
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                                                                                                                                                           Matches
                                                                                                                                                                                     Query Match
                                                                                                                                                                        Best Local
                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 VFYAFSFPLHVVXNPIARFYSVFALIDEAYAVTAARP---AGWSAWRLISMQIAFHSYWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224
                                                          130 FALIDEAYAV-----TAARPA--GWSAWRLISMQIAFHSYWVFGGLTGVAIAELIPF- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 IGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIA-LVVGAAPLGAIALTTLLVNFRH 107
180 EIKGLEFALCSLFV---TLTLDSCRTKKQIPSLLLAGLSF---TIALVVIPGQAL-FAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
52; Conser
                              77 TLLTDESFALGMNKLNHTKGRLSFEWFNAANLIS----YATWVFSTIIGAYLGRFTANP 131
                                                                                                               71 SGLIPAGSTEMLVIALVVGAAPLGAIALTTLLVNFRHVFYAFSF-PLHVVKNPIARFYSV 129
                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGVTAGYFIGSAIPDPKTFGLDAIFPAILIALTFSALKNK---VTRKAAFAGSTLALITT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGGLTGVAIAELIPF-EIKGLEFALCSLFVTLTLDSCRTKKQIPSLLLAGLSFTIALVVI 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPFGIAVN-EMIRGKFSOYFGSHIMNDESVLFGMAQPDFETKKAAYWLCGIGIMLS--WP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGMSLGSLAASYGLALWIPLCLSIFVLAGTAEFIFIGFLAVGGSPIAA-AIAGLLVNLRH
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                                                                                              SPFIFAGSAQFVTVSMLTGGSFILSIVLATFLVNARMILMGMTIAPYFKAESLGKNLWLG
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26.4%; Pre
ative 37;
                                                                                                                                                                      10.8%; Score 137; DB 4
26.8%; Pred. No. 1e-07;
                                                                                                                                                            42;
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Pred. No. 4.1e-08;
"" wiematches 95;
                                                                                                                                                            Mismatches
                                                                                                                                                                                         DB 4; Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                               ACID SEQUENCES RELATING FOR DIAGNOSTICS AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32299
LENGTH: 484
Type: perm
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US-09-543-681A-4173
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Sequence 32299, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
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US-09-543-681A-4173
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                                                            US-09-252-991A-32299
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Best Local S
Matches 56
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SEQ ID NO 4173
LENGTH: 230
TYPE: PRT
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
Query Match
Best Local Similarity
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                                                                               ORGANISM: Pseudomonas
                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 AIALTTILVNFRHVFYAFSFPLHVVKNP---IARFYSVFALIDEAYAV-----TAA--RP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 LLVSLADGI----VGISYGALAHTQGFDFWVPLSLSIFVLAGASEFLFIGVVAMGGSAIY 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 LKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALV-VGAAPLG
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56; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGWSAWRLISMQIAFHSYWVFGGLTGVAIAE-LIPFEIKGLEFALCSLFVTLTLDSCRTK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A-ALAGLMVNARHI----PFSMAVKELPGKGIKSLLGFHILNDESVVFGLSQSTAEQNRL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KQIPSLLLAGLSFTIALVVIPGQALFAALLIFLGLLTI 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.6%; Score 134.5; DB 4 ilarity 25.7%; Pred. No. 2.4e-07; Conservative 42; Mismatches 91
  8.9%;
25.1%;
                                                                               aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPLGTMLGVYLGSFIVDIKMLGLDAMFPAIILALSLPALKNK 190
  Score 113.5; DB 4; Pred. No. 0.00018;
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                   Length 484;
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18185
SEQ ID NO 18185
LENGTH: 270
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US-09-252-991A-18185
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Best Local S
Matches 69
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marc J.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116
                                                                                                                                                                                     100 TLLVNFRHVFYAFSFPLHVVKNPIARFYSVFALIDEAYAVTÁARFAGWSAWRLISMQIAF 159
205 GL-----FILAGLYAAREPWLLAACLLPGMAL
                                                                                                              160 HSYW-----VFGGLTG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 IAQG----LKTSLAAGLG-MYPIGIAFGLLVIQYGYEWWAAPL----
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                                                                                                                                                                                                                                                                                                                                                                                   69;
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALY-----CFGALL
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                                                                                                                                                                                                                                                                                                                                          SSLEVSPSKAALEPDDKGYRRYEIAQGLKTSLAAGLGMYPIGIA-FGLLVIQYGYEWWAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALVVIPGQALFAALL 233
                                    TLDSCRTKKQIPSLLLAGL----SFTIALVVIPGQAL
                                                                                                                                                     ALRAEL-----LMLALGVFVSFYALYALF-----LQPRGQPRWR
                                                                                                                                                                                                                            PLLAGVLPLSQIIPLLVLLDFSASFGNWLPARRQIAVTELKRLLPCMLLGCA-LGAYGLL 115
                                                                                                                                                                                                                                                                 PLFSGLI-----FAGS-----TEM--LVIALVVGAAPLGAIALT 99
                                                                         -ATWALPFGVPGGLFGALFGSGGFLYSLYLNGRLASKE----QMRATQSALIGCSTFVRL
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                                                                                                                                                                                                                                                                                                                                                                               8.4%; Score 106; DB 4; Length 270; ilarity 24.8%; Pred. No. 0.00059; Conservative 29; Mismatches 64; Indels 1
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                -----VAIAELIPFEIKGLEFAL--CSLFVTL 195
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    231
                                      228
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RESULT 15 US-09-252-991A-31521 ; Sequence 31521, Ap

Application US/09252991A

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Search completed: April 16, 2004, 06:56:34
Job time: 24.7716 secs
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERENCE: 107.26.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31521

LENGTH: 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.2%; Score 104; DB 4; Length 555; Best Local Similarity 22.1%; Pred. No. 0.0028; Matches 75; Conservative 32; Mismatches 92; Indels 140; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 LCMGLVALLLPWLGRWLAEHRGIVCGLLAIAAAC-LWRLELDSGLALIASAALAGSGVAI 274
                                                                                                                                                                                                                         446 CGLL---LMPLQHAALMVALIGYGLGACFALSLTLTLDHLHEPRAAGSLAAFVQGIGFII 502
                                                                                                                                                                                                                                                                                                                                                                                      335 LLA---LLLWMFARPREVLPSAGEGFVRHFFGNRRGWLLAVYFGLINGGYTSMVAWLPVY 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 LLVNFRHVFYAFSFPLHVV----KNPIARFYS-----VFALIDEAYAVTAA----- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 IQALVPGVVKRWFPRRVPAAMGLYSASLMAGGGTAAVLSPRIAEHFSNWQAGLGAWAVPA 334
                                                                                                             503 TGIVPYLTGWLRDVTGSFQASWLLLAASVVAMLLVTLRF 541
                                                                                                                                                                                                                                                                           169 TGVAIAELIPFEIKGLEFAL-----C-SLFVTLTLDSCRTKKQIPSL--LLAGLSFTI 218
                                                                                                                                                                                                                                                                                                                                         392 YRQLGWSAQDSGGLVGIMTIFQVLAALSVPLLIRRRLDRRPWLLAALLVQ------LGGF 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 VIALVVGA-----APLGAIALTT 100
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                                                                                                                                                                      ALVV------IPGQ-----ALFAALLIFLGLLTIRY 243
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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161.5
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Match Length
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1269
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| cgn2_6/ptcdata/1/paa/USO6_NEW_COMB.pep:*
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| cgn2_6/ptcdata/1/paa/USO8_NEW_COMB.pep:*
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     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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             US-10-417-894A-4920
US-10-724-972A-6721
US-60-556-841-7285
PCT-US04-03417-32
US-10-725-081-14
US-60-556-857-097C-148
US-09-857-097C-149
US-09-857-097C-150
US-09-857-097C-150
US-09-857-097C-150
US-09-857-097C-150
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US-10-417-884A-3665
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US-10-781-014-659
US-10-7856-841-12104
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US-10-7856-841-10192
US-60-556-841-0192
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Sequence 4920, Ap

Sequence 2490, Ap

Sequence 2490, Ap

Sequence 32, Appl

Sequence 32, Appl

Sequence 14, Appl

Sequence 14, Appl

Sequence 148, Appl

Sequence 150, App

Sequence 152, App

Sequence 152, App

Sequence 2463, App

Sequence 232, App

Sequence 6176, App

Sequence 6176, App

Sequence 6176, App

Sequence 6176, App

Sequence 6176, App

Sequence 6176, App

Sequence 6176, App

Sequence 6176, App

Sequence 10192, App

Sequence 7076, App

Sequence 7076, App

Sequence 7076, App

Sequence 4257, App

Sequence 10192, App

Sequence 10192, App

Sequence 7076, App

Sequence 7076, App

Sequence 44, Appli
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US-10-417-884A-4920
                                     FEATURE:
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ALIGNMENTS

S-QUENCE 4920, Application US/10417884A
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS

CORRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: WALLHAM
STATE: MASSACHUSETTS
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: DUROM ISO9660
COMPUTER READABLE FORM:
MEDIUM TYPE: DUROM ISO9660
COMPUTER P. C
OMERATING SYSTEM: US/10/417,884A
APPLICATION NUMBER: US/09/107,532
FILING DATE: 17-Apr-2003
PRIOR APPLICATION NUMBER: US/09/107,532
FILING DATE: 17-Apr-2003
APPLICATION NUMBER: US/09/107,532
FILING DATE: 17-Apr-2003
APPLICATION NUMBER: 05/085,598
FILING DATE: 17-Apr-2003
APPLICATION NUMBER: 05/085,598
FILING DATE: 17-Apr-2003
APPLICATION NUMBER: 05/085,598
FILING DATE: 17-Apr-2003
APPLICATION NUMBER: 05/055,71
FILING DATE: 14 May 1999
APPLICATION NUMBER: 05/055,591
FILING DATE: 14 May 1999
APPLICATION NUMBER: 05/055,591
FILING DATE: 14 May 1999
APPLICATION NUMBER: 05/055,591
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APPLICATION

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PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-134,001
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: 60/64,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: 60/055,779
PRIOR APPLICATION NUMBER: 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 7544
SEQ ID NO 6721
LENGTH: 242
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US-10-724-972A-6721
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                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT; ORGANISM: S.epidermidis
US-10-724-972A-6721
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Best Local
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CURRENT APPLICATION NUMBER: US/10/724,972A
CURRENT FILING DATE: 2003-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Doucette-Stamm, Lynn
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                             ch 12.7%; Score 161.5; DB 6; Length 242; 1 Similarity 24.8%; Pred. No. 2.4e-09; 1 Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --LGLLTIRYFF
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                           SQFEGIKKSRLRIYIVLIVCVIVMMLLLSSILPSYVAILI--AAIVAALL 236
                                                                                                                                                                                                                                                                                                         QGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGSAQFITVSMLASHSPLLSIVFSTFLVNSRMILMSMTIAPYFKKNRLLQNLLIGTLLTD 130
                                                                                                        KGEKINDRW----LHGLNITAYLFWTVSCVIGAIFGEYISNPDALGLDFAITAMFIFLCI
                                                                                                                                             ----AGWSAWRLISMQIAFHSYWVFGGLTGVAIAELIPF-EIKGLEFALCSLFVTLTL 197
                                                                                                                                                                                                                                                                  ÓGVKECIPTLÍGYAGVGLSFGIVAASQNFSVLEIILLCLIÍYÁGAAQFIICTLVIAGTÞI
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                                                              --IPSLLLAGLSFTIALVVIPGQALFAALL 233
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US-60-556-841-7285
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; ORGANISM: Bacillus halodurans
US-60-556-841-2490
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US-60-556-841-2490
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                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Ferroplasma acidarmanus US-60-556-841-7285
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GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)
CURRENT APPLICATION UNMEER: US/60/556,841
CURRENT FILING DATE: 2004-03-25
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 12463
SEQ ID NO 7285
LENGTH: 477
TYPE: PRT
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SEQ ID NO 2490
LENGTH: 455
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GENERAL INFORMATION:
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Best Local :
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TITLE OF INVENTION: Genes and Uses for Plant
FILE REFERENCE: 38-21(53450)
CURRENT APPLICATION NUMBER: US/60/556,841
CURRENT FILING DATE: 2004-03-25
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Local Similarity 27.5%;
hes 56; Conservative 2
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                       SYWVFGGLTGVA----IAELIPFEIKGLEFALCSLFVTLTLDSCRTKKQIPSLLLAGLS
                                                                                   VAVGMVLAIFS--MSGSSAVVTLGEEAQQPRKNIKKALLISFITTGVVFVLTSYALTVGW 262
                                                                                                                         RLISMQIAFHSYWVFGGLTGVAIAE------LIPFEIKGLEFALCSLFVT---
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; Pred. No. 0.017;
26; Mismatches 6
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; Pred. No. 0.023;
31; Mismatches 8
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; ORGANISM: Homo sapiens
PCT-US04-03417-32
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PRIOR FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US 60/448,389
PRIOR FILING DATE: 2003-02-18
PRIOR FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/456,320
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 60/460,279
PRIOR FILING DATE: 2003-04-03
PRIOR PRIOR PRIOR DATE: 2003-04-03
PRIOR FILING DATE: 2003-04-28
PRIOR FILING DATE: 2003-04-28
PRIOR FILING DATE: 2003-04-28
                                                                                                           US-10-772-636-32
Sequence 32, Application US/10772636
GENERAL INFORMATION:
APPLICANT: Kelly, Louise M.
APPLICANT: Carroll, Joseph M.
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Best Local Similarity
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SEQ ID NO 32
LENGTH: 760
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CURRENT FILING DATE: 2004-02-05
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APPLICATION NUMBER: US 60/498,106
FILING DATE: 2003-08-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                   TLTLDSCRTKK-----QIPSLLLAGLSFTIALVVIP 224
                                                                                                                                                                                                                                                                                                                        AFTLRSINPFGNS --RLVLFYVEYHTPWY------MAELFPFILLGVFGGLWGTLFI
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Healy, Aileen
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US-10-725-081-14

Sequence 14, Application US/10725081 GENERAL INFORMATION:

APPLICANT: ADLER, JON ELLIOT APPLICANT: ZOZULYA, SERGEY APPLICANT: LI, XIADONG

APPLICANT: ZOZULYA, SERGEY
APPLICANT: LI, XIADONG
APPLICANT: LI, XIADONG
APPLICANT: O'CONNELL, SHAWN
APPLICANT: STASZEWSKI, LENA
TITLE OF INVENTION: TAR TASTE RECEPTORS AND
FILE REFERENCE: 078003/0277870/RXT
CURRENT APPLICATION NUMBER: US/10/725,081
CURRENT APPLICATION UNBER: US/10/725,081
CURRENT FILING DATE: 2003-12-02

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APPLICATION NUMBER: 60/187,546 FILING DATE: 2000-03-07

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CURRENT APPLICATION NUMBER: US/10/772,636
CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US 60/445,241
PRIOR FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US 60/448,389
PRIOR FILING DATE: 2003-02-18
PRIOR FILING DATE: 2003-02-18
PRIOR FILING DATE: 2003-02-19
PRIOR FILING DATE: 2003-02-79
PRIOR FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US 60/460,279
PRIOR APPLICATION NUMBER: US 60/465,924
PRIOR APPLICATION NUMBER: US 60/465,924
PRIOR FILING DATE: 2003-04-28
PRIOR FILING DATE: 2003-04-28
PRIOR FILING DATE: 2003-04-28
PRIOR FILING DATE: 2003-04-28
PRIOR FILING DATE: 2003-04-28
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Best Local
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APPLICANT: Healy, Alleen
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: HEMATCLOGICAL DISORDERS USING 9118, 990, 1760
TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 536
TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943,
TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 2846
TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, TITLE OF INVENTION: 5014
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PRIOR FILING DATE: 2003-05-13
PRIOR APPLICATION NUMBER: US 60/498,106
PRIOR FILING DATE: 2003-08-26
PRIOR PRIOR PRIOR DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US 60/500,179
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PRIOR FILING DATE: 2003-09-15
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ORGANISM: Homo
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351 RCNIAWCRRRKTTRLGKYPVLEVIVVTAITAIIAYP 386
                                                                                                                301 AAFTLRSINÞFĠNŚ--RLVLFYVEYHTÞWY--
                                                                                                                                                               135 EAYAVTAARPAGWSAWRLISMQIAEHSYWVFGGLTGVAIAELIPFEIKGLEFALC-SLFV 193
                                                                                                                                                                                                                             254 EVLSAAAAAGVSVAFGAPIGGV----LFSLEEVSY--YFPLKTL-----
                                                        194 TLTLDSCRTKK-----QIPSLLLAGLSFTIALVVIP 224
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Pred. No. 0.042;
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; PRIOR FILING DATE: 2001-01-03; NUMBER OF SEQ ID NOS: 20; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 14; SEQ ID NO 14; LENGTH: 658; TYPE: PRT; CRGANISM: Rattus sp. US-10-725-081-14
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US-60-554-751-14
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                                                                                                                                                                                                                              ) ORGANISM: Rattus rattus US-60-554-751-14
                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/60/554,751
CURRENT FILING DATE: 2004-03-19
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PACENTIN VERSION 3.2
SEQ ID NO 14
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/60554751
GENERAL INFORMATION:
APPLICANT: Li, Xia
APPLICANT: Li, Weihua
APPLICANT: Reed, Danielle R.
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Best Local Similarity
Matches 59; Conserv
                                                                                                                                                 Matches
                                                                                                                                                                  Query Match 7.7%;
Best Local Similarity 22.3%;
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PRIOR APPLICATION NUMBER: 60/214,213
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 30/226,448
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 60/259,227
PRIOR APPLICATION NUMBER: 60/259,227
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reed, Danielle R.
APPLICANT: Bachmanov, Alexander A.
APPLICANT: Brand, Joseph G.
TITLE OF INVENTION: TASTE RECEPTOR OF THE TIR FAMILY FROM DOMESTIC
FILE REFERENCE: MON-0298
                                                                                                                                                                                                                                                                       LENGTH: 858
TYPE: PRT
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FILING DATE: 2000-04-07
APPLICATION NUMBER: 60/209,840
FILING DATE: 2000-06-06
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                             95
                                                                                                           52 AFGLLVIQYGYEWWAAPLFS------
                             AIALT----TLLVNFRHVFYAFSFPL---
                                                                    ALGLTV-----HYWDSPLVQASGGSLFCFGLICLGLFCLSVLLFPGRPRSASCLAQQPMA 645
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                                                                                                                                                 Conservative
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                                                                                                                                                 35;
                                                                                                                                                                  Score 98; DB 7;
Pred. No. 0.048;
                                                                                                                                                     Mismatches
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; FEATURE:
; OTHER INFORMATION: RhCE Residues 111-125
US-09-857-097C-148
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US-09-857-097C-148
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US-09-857-097C-149
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PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 152
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 148
LENGTH: 417
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Best Local (
                                                                                                                    Sequence 149, Application US/09857097C GENERAL INFORMATION:
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APPLICANT: Barker, Robert, N.
TITLE OF INVENTION: ALLO- AND AUTO-REACTIVE
FILE REFERENCE: P097
CURRENT APPLICATION NUMBER: US/09/857,097C
CURRENT FILING DATE: 2001-05-31
APPLICANT: Urbaniak, Stanislaw J.
APPLICANT: Barker, Robert, N.
TITLE OF INVENTION: ALLO- AND AUTO-REACTIVE
FILE REFERENCE: P097
CURRENT APPLICATION NUMBER: US/09/857,097C
CURRENT FILING DATE: 2001-05-31
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21.7%; Pred. No. 0.028;
vative 41; Mismatches 90;
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PRIOR APPLICATION NUMBER: 9826378.3
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 152
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 150
LENGTH: 417
TYPE: PRT
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US-09-857-097C-150
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Best Local S
Matches 65
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PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 152
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 149
LENGTH: 417
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                                                                                                                                                                                              Query Match
Best Local Similarity
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APPLICANT: Barker, Robert, N.
TITLE OF INVENTION: ALLO- AND AUTO-REACTIVE T-CELL
FILE REFERENCE: P097
                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/857,097C CURRENT FILING DATE: 2001-05-31
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                               OTHER INFORMATION: RhcE Residues 131-145
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l Similarity 21.7%;
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IAL-----AREYSVEALI 133
                                                                                                                  ASLE-DOKGLVASYQVGQDLTVMAALGLGFLTSNFRRHSWSSVAFNLFMLALGVQW--AI 92
                                                                                                                                               AALEPDDKG-YRRYEIAQGLKTSLAAGLGMYP-----IGIAFGLLVIQYGYEWWAAP
                                                  LLDGFLSQFPPGKVVITLFSIRLATMSAMSVLÍSÁGAVLGKVNLAQLVVMVLVEVTALGT 152
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                                                                                                                                                                              7.6%; Score 96.5; I
21.7%; Pred. No. 0.02
htive 41; Mismatches
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                                                                                                                                                                                   103;
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US-09-857-097C-152
Sequence 152, Application US/09857097C
GENERAL INFORMATION:
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US-10-417-884A-3665
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Best Local S
Matches 65
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SEQ ID NO 152
LENGTH: 417
                                                                                                                                                    Sequence 3665, Application US/10417884A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Barker, Robert, N.
TITLE OF INVENTION: ALLO- AND AUTO-REACTIVE
FILE REFERENCE: P097
CURRENT APPLICATION NUMBER: US/09/857,097C
CURRENT FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 9826378.3
PRIOR APPLICATION NUMBER: 9826378.3
PRIOR PILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Urbaniak, Stanislaw J. APPLICANT: Barker, Robert, N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                             NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                      APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 DEAYAVTAARPAGWSAWRLISMQI-----AFHSYWVFGGLTGVAIAELIPFEIKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AALEPDDKG-YRRYEIAQGLKTSLAAGLGMYP-----IGIAFGLLVIQYGYEWWAAP
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                                                                                                                                                                                                                                                                 SSLAHPORKISMT-----YVHSAVLAGGVAVGTSCHLIPSPWLAMVLGLVAGLISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASLE-DOKGLVASYOVGODLTVMAALGLGFLTSNFRRHSWSSVAFNLFMLALGVQW--AI
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                                                                                                                                                                                                                                                                                                                                                                                                              LRMVISNIFNTDYHMNLRH-FYVFAAYFGLTVAWCLPKPLPKGTEDNDQRATIPSLSAML
STATE: Massachusetts
                                    STREET:
                 CITY: Waltham
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                                  100 Beaver Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LIFAGST-----EMLVIALVVGAAPLGA
                                                                                                     and David Bush
AND AMINO ACID SEQUENCES RELATING
FAECIUM FOR DIAGNOSTICS AND THERAP
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COMPUTER READABLE

MEDIUM TYPE:

CD/ROM ISO9660

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                                                                                                                                                                                                                                                                                                                          RESULT 14
US-60-556-841-2463
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                                                                           ; ORGANISM: Brassica rapa
US-60-556-841-2463
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Best Local Simi
Matches 34;
                                                                                                                                                                                       Sequence 2463, Application US/60556841
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant
FILE REFERENCE: 38-21(53450)
CURRENT APPLICATION NUMBER: US/60/556,841
CURRENT FILING DATE: 2004-03-25
  Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                NUMBER OF SEQ ID NOS: 12463
SEQ ID NO 2463
LENGTH: 389
TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: ATITICLEO, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA
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LOCATION: (B) LOCATION 1...326
SEQUENCE DESCRIPTION: SEQ ID NO: 3665:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 RPAGWSAW-RLISMQIAFHSYWVFGGLTGVAIAELIPFEIKGLEFAL------CSLFV 193
                                                                                                                                                                                                                                                                                                                                                                                                         126 GTLLFLSLTRL---FLQK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 TLTLDSC-----RTKKQIPSLLLAG-----LSFTIALVVIPGQAL------FA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
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Similarity 24.6%;
34; Conservative 2
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APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
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FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085,598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 326 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (781)893-50
TELEFAX: (781)893-8277
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7.2%; Score 91.5; DB 7; illarity 23.3%; Pred. No. 0.087; Conservative 28; Mismatches 90;
                                                                                                                                                                                                                                                                                                       Application US/60556841
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                                                                                                                                                                                                                                                  Improvement
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                                        Length 389;
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      Indels
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      Gaps
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CURRENT APPLICATION NUMBER: US/09/857,097C
CURRENT FILLING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 9826378.3
PRIOR FILLING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 152
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 151
LENGTH: 417
TYPE: PRT
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Search completed: April 16, Job time: 18.4791 secs
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GENERAL INFORMATION:
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APPLICANT: Barker, Robert, N.
TITLE OF INVENTION: ALLO- AND AUTO-REACTIVE T-CELL EPITOPES
FILE REFERENCE: P097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MQIAFHSY------WVFGGLTGVAIAELIPFEIKGLEFALCS--LFVTLTLDSCRTK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLGMYPIGIAFGLLVIQYGYEWWA-----APLFSGLIFAGS--TEMLVIALVVGAAPLG
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                                                                                                                                        VHSAVLAGGVAVGTSCHLIPSPWLAMVLGLVAGLISVGGAKYLPGCCNRVLGIPHSSIMG
                                                                                                                                                                                                              ALFLWIFWPSFNSALLRSPIERKNAVF---NTYYAVAVSVVTAISGSSLAHPQGKISKTY
                                                                                                                                                                                                                                                                                      LRMVISNIFNTDYHMMMHIYVFAAYFGLSVAWCLPKPLPEGTEDNDQTATIPSLSAMLG
                                                                                                                                                                            FHSYMVFGGLTGVAIAELIPFE----IKGLEFALCSLFVTLTLDSCRTK-KQIPSLLLAG
                                                                       YNF--SLIGILGEIIYIVLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.1%; Score 90; DB 5; ilarity 21.5%; Pred. No. 0.14; Conservative 36; Mismatches 10
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Best Loo Matches Qy Db Db	ORIGIN	JOURNAL COMMENT COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	RESULT 15 CK295424 LOCUS DEFINITION	00 QQ DD QQ
Sal Similarity 47.5%; Fred. No. 26; 103; Conservative 0; Mismatches 114; Indels 74 TTCCGTTCTTAATCCTTAAGCCCCTACGTGAATCACAATTTGTGGGCAAAA 74 TTCTAATCTTAATCGTCAGCCCGAAAACATCTCAAGGTGGGCGGAAAA 419 TTCTAATCTTAATCGGTCAGCCCGAAAAACATCTCAAGGTGGGCGGGAAAA 1134 GGATGCCAAGGAATCCTTGCCATTTGACCGCATCAACGTTTCGAGCAGCA 1134 GGATGCCAACGAAGTGTTTCATTTGCTTTGGAATTCCCAATTATGAAGT	/organism="Micordata benderic for the state of the state	Unpublished (2003) Other_ESTs: EST758139 Other_ESTs: EST758139 Contact: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850 Email: potato-array@tigr.org Clones can be requested from TIGR via potat Seq primer: ATT TAG GTG ACA CTA TAG. Seq primer: ATT TAG GTG ACA CTA TAG. Seq primer: ATT TAG GTG ACA CTA TAG. 1936 Ce 1936 Ce 1936 Ce 1936 Ce 1936 Ce 2	end, mRNA sequence CK295424.1 GI:398 EST. Nicotiana benthami Nicotiana benthami Eukaryota; Viridi Spermatophyta; Mac asterids; lamiids asterids; lamiids 1 (bases 1 to 938 Buell, C.R., Hart, Stankawicz B., Jim	CK29	555 GGATGATACCACAAGTGTTTTCATTTGCTTTGGAATTCCCAATTATGAAGTTTTTTGCAAG 614 194 ATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTGGTGGCGCATCTTC 253 1

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1 (bases 1 to 890)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.

Generation of EST sequences from Nicotiana benthamiana
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; 
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; 
asterids; lamiids; Solanales; Solanaceae; Nicotiana.
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CK288648
CK288648.1 GI:39866370
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EST751370 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMBI02 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
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The Institute for Genomic Research
9712 Medical Center Dr, Rockville,
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TTCTAATGTTAATCGGTCAGCCCGAAAAACATCTCAAGGTGGGCGGGGAAATTCGCGCGCTGT
                                            rrccerrcraarccraaeccccracereaarcacaarrrereeccaaareecearer 133
                                                                                             Conservative
                                                                                                                                                                                                                 /clone lib="Micotiana benthamiana mixed tissue cDNA library, normalized, full-length" /note="Vector: pcfw/Sport6.1; Site 1: EcoR; Site 2: Not1; /note="Vector: pcfw/Sport6.1; Site 1: EcoR; Site 2: Not1; /note="Vector: pcfw/Sport6.1; Site 1: EcoR; Site 2: Not1; /note="Vector: pcfw/Sport6.1; Site 1: EcoR; Site 2: Not1; /note = "Vector: pcfw/Sport6.1; Site 1: EcoR; Site 2: Not1; /note = "Vector: pcfw/Sport6.1; /note = from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). NA was isolated from these tissues and pooled in approximately equal molar amounts."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
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/mol_type="mRNA"
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REFERENCE
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Matches 103
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Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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StasKawicz,B., Jin,H. and Baker,B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other_ESTE: EST75859
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Nicotiana benthamiana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 922)

1 (bases 1 to 922)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research 9712 Medical Center Dr, Rockville,
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end, mRNA sequence.
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                                                                                                                                   /Clone lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length" /note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (3 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar
                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-TonA"
                                                                                                                    campestris pv vesicatoria 18 these tissues and pooled in amounts."
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/db_xref="taxon:4100"
/clone="NBMCX72"
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                       10.7%;
Score 34.6; DE Pred. No. 26; 0; Mismatches
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                                                 DB 14;
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                                              Length
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2003)
Contact: Martin FM
Equipe de Microbiologie Forestiere
Institut National de la Recherche Agronomique
Centre INRA de Nancy, 54280 Champenoux, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               x Populus deltoides CDM
CB239541
CB239541.1 GI:30233030
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kohler, A., Delaruelle, C., Martin, D. and Martin, F. The poplar root transcriptome: analysis of 7000 expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Populus balsamifera subsp. trichocarpa x Populus deltoides Populus balsamifera subsp. trichocarpa x Populus deltoides Populus balsamifera subsp. trichocarpa x Populus Bultoides Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +33 383 39 40 80 Fax: +33 383 39 40 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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/dev_stage="two-month-old"
/clone_lib="two-month-old roots from clone 'Beaupre' grown for 19 days under restricted irrigation"
/note="Organ: root; Vector: pTriphEx2; cDNA library of roots from two-month-old Populus trichocarpa Torr.& Gray x deltoides Bartr. Ex Marshall (clone 'Beaupre') grown for 19 days under restricted irrigation to reach 50% of the transpiration rate of fully watered plants. The cDNA library was constructed from 1 ug of total RNA using the SMART cDNA synthesis kit (Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. The resulting cDNA was packed into lambda phages using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="loomo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Populus balsamifera subsp. trichocarpa Populus deltoides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 'mol_type="mRNA"
'cultivar="'Beaupre'"
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39.9%; Pre
ative 25;
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1 (bases 1 to 853)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.

Generation of EST sequences from Nicotiana benthamiana Unpublished (2003)

Other ESTs: EST760192

Other ESTs: EST760192
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EST760191 Nicotiana benthamiana mixed tissue cDNA library,
Nicotiana benthamiana cDNA clone NBMD912 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST.
Nicotiana benthamiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seg primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       normalized, full-length Nicotiana benthamiana cDNA clone
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/clone lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length" /note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI; supplier: RNA was isolated from NIcotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (5 C3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; and Xanthomonas campestris pv campestris 12 hr, 18hr; and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gigapack III Gold packaging kit (Stratagene, La Jolla, CA). The pTripLEx2 phagemid clones in Escherichia choli were obtained by using the mass in vivo excision protocol according to the manufacturer's instructions (Clontech)."
                                                                                                                                                                                                                                                                                                         /tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"
/lab_host="DH10B-TonA"
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Nicotiana benthamiana"
|mol_type="mmNa"
|/mbl_type="mmNa"
|/db_xref="teaxon:4100"
|/clone="NBMD912"
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Query Match Best Local Similarity Matches 103; Conserv

10.7%;

Score 34.6; DI Pred. No. 25; 0; Mismatches

DB 14; 114;

Length 853; Indels

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Gaps

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Query Match
Best Local :
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RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse frequenced and sequence Laboratory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new
                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri (Dases 1 to 808)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (Unpublished (1999)
                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                         808 bp 602907255F1 NCI_CGAP_Kid14 Mus r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues
Bmail: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
cDNA Library Preparation: Life Technologies,
                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                       BI144284
BI144284.1 GI:14604285
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACATCTGTGTTGCCAGCCCTCCTTCTTGTGCGTGTGTGCTAAGGCCATGCTTTCTGT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCCTGGCACCATCGTTTTTGT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGACGTAGCTGATCTTTTAATCCCTTGGTGTAAGCTGCTGGTTGTTAGCAGAGCTGGTGC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTGGTGGCGC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="F830034E14"
/tissue_type="activated spleen"
/clone_lib="kIKEN full-length en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain="NOD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers,
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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BX387771
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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ORIGIN

Matches

REFERENCE AUTHORS

TITLE JOURNAL

RESULT 9 BI144284

ACCESSION VERSION

KEYWORDS

DEFINITION

SOURCE ORGANISM

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SOURCE
ORGANISM
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                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 GAICTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTGGTGGCGCATCTT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              523 TGGAGGCCTCCATGGTTCCAACTTTATGTGCAGCCAGACTGGGACATCAACAAGCAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 Гебалессавсаватсствесатттвассветсь сттессавса поставовать 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9X387771 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens CDNA clone CSODIO52YB18 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 6
High quality sequence stop: 793.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11173 row: m column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li, W.B., Gruber, C., Jessee, J. a Full-length cDNA libraries and Unpublished (2001)
                                                                                                                                                                                           http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOAIO52DA09QP1&cluster=4682.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
                                                                                                                                                                                                                                                                              Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4682.r
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                         Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX387771.1 GI:30460721
                                                                                                           http://fulllength.invitrogen.com/
Faraday Avenue Genoscope sequence
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTGGCAATAGGCG 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTGGCGGTCGACG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTCAGAGGATAGAAGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:5064373"
/lab host="DH108 (Ti phage-resistant)"
/lab host="NOI COAP Kid14"
/clone lib="NOI COAP Kid14"
/note="Organ: kidney; vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: kidney; vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Sycrage insert size 1.75 kb. Constructed by Life
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mol_type="mRNA"
strain="FVB/N"
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Pred. No. 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Polayes,D.
d normalization
                                                                                                                                        InVitroGen Corporation 1600 ID : CSOAIO52DA09QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 08-MAY-2003
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REFERENCE
AUTHORS
TITLE
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VERSION
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                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                      FEATURES
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Best Local S
Matches 64
                                                                             Best Local
Matches
                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                               Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Biffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACFAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272
847
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                                      29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1+Y), genomic
AL056828
                                                                          l Similarity 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL056828.1 GI:4937496 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNS00BD8 1101 bp DNA linear GSS 04 Drosophila melanogaster genome survey sequence TET3 end of BACR23H11 of RPCI-98 library from Drosophila melanogaster [1], genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATOTGACGGOTCAAATOTOTTTCCCCAATCCGACATCGCGCACGGTGGCGCCGCGCGCCC 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTTTTT 303
TTGSGKTGGTTGSGTAASDTGTTTATATTSTTTTBSKBTSTBTSKNAATKTWSASSTTTT 906
                   TIGITGICGCAGIATGICGCICAGICATIACTITIGCGCICCGGGCGGTICCGTICTIAATCC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGTTGCGGCGATCCTCGCTGGCGAACGACCGCGATGGCTGCCCCGTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.9%;
milarity 57.1%;
Conservative
                                                                        10.9%;
ilarity 24.4%;
Conservative 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="B73"
/db_xref="taxon:4577"
/clone="ZwMSTa530007"
/clone = "Ibb="ZM, 0.6 1.0 KB"
/note="Vector: pcR4-TOPO; Site_1: E/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submission
                                                                                                                                                                         /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="texon:727"
/clone="BACR23H11"
/clone_"BACR23H10"
/clone_lb="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 35.2; L
; Pred. No. 17;
0; Mismatches
                                                                          ; Score 35.2; DB 29; pred. No. 18; 81; Mismatches 111;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutereo; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Wuridae; Murinae; Mus.

Okazaki, Y., Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Kiyosawa, H., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Kiyosawa, H., Oshori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T. A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T.,

Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T. A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T.,

Gustincich, S., Hirokawa, N., Jackson, I.J., Drayani, T. A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B.L., Konaggaya, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B.L., Konaggaya, A.,

Kawaji, H., Kawasawa, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Rayasi, T., Reed, J.C., Reed, D.J., Raid, J., Ramachandran, S.,

Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,

Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zinmer, A., Carninci, P.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zinmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Shinagawa, J., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Sakai, K., Sakai, K., Sasaki, D., Shibata, K.,

Sakai, K., Sakai, K., Sakai, K., Sasaki, D., Shibata, K.,

Sakai, S., Sakai, S., Hara, A., Hashizume, W., Impara, M.,

Sakai, S., Sakai, S.
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                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group,
Sciences Genter (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (I
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa
Tel: 81-45-503-9222
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Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/Adachi,J., Aizawa,K., Akimura,T.,
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Sciurognathi; Muridae; Murinae; Mus.
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na, Kanagawa 230-0045, Japan
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Arakawa, T., Carninci, P.,

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     REFERENCE
AUTHORS
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1 (bases 1 to 475)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                           Zea mays
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

l (bases 1 to 786)
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CF338060.1 GI:33824491
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     Whitelaw, C.A., Quackenbush, J., Van Aken, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACGGCCTTCAGAGAGCCATTCTTCTGATGCTTCTCTCTGCTCTGTTCT
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82 31 321 6355
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/lab_host="E-Coli DH108"
/clome lib-"AtcMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="JMT--08-M05"
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        Utterback, T.,
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PUHTK88TD ZM 0.6_1.0_KB Z
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CC362201.1 GI:30831601
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                                                                                                                                                                                                                                                                                                              Maize Genomics Consortium Unpublished (2003) Other GSSs: PUHTK88TB
                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
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Class: sheared ends.
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Fax: 301-838-0208
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9712 Medical Center Drive,
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Unpublished (2003)
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                                                                                                              Class: sheared ends.
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/clone="zMMBTA137A09"
/clone lib="ZM_0.6 1.0 KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pacs1-60 663.81 pacs1-60 Pseudomonas a pacs1-60-663, genomic survey sequence. 82557685
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Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M., Spuncer,D.H., Raul,R. and Olsen,M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas acruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                     Box 352145, Seattle, Tel: 2062216954
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                     University of Washington
                                                                                                                                                                                                                                                                                                                                                               Contact: Chris K. Raymond
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                                                                                                                                                                                                                        shotgun
                                                                                                                                                                                                                                          craymond@u.washington
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR12G04"
/clone=lib="RPCI-98"
/note="end : TET3"
                 library."
                                  /clone="pacs1-60_663"
/clone_lib="pacs1-60"
/note="clinical isolate 1-60 Whole
                                                                                                                                                         /organism="Pseudomonas
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                                                                                                     /db xref="taxon:287"
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104
                               171 AACGITTCGCAGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCT 218
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF302597
7LEAF--08-E15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--08-E15, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics and Genetics Institute, GreenGene Biotech II of Bioscience and Bioinformatics, Myongdi University Yongin, Kyoenggi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                       /db xref="taxon:4530"
/clone="71EAF-08-EL5"
/clone="71EAF-08-EL5"
/tissue_type="1eaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DHIOB"
/clone_lib="Rice_leaf_plasmid_cDNA_library_II_(7LEAF)"
/clone_lib="Rice_leaf_plasmid_cDNA_library_II_(7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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CF302597 7LEAF--08
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8283	CF58283	38	0	N	44
0763	BF20763	2	0	N	43
0191	BI90191	65	0	N	42
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3484	BI13484	96	0	N	40
3520	BI13520	86 1	0	N	39
6079	BF46079	69]	0	N	ω 8
8906	AW48906	63	0	32.8	37
5774	AW45774	16 1	0	N	36
9178	AW49178	99 1	0	N	ω 5
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5768	BZ557	62		4	19
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213	CK292	51	0:	4	16
9542	CK295	36 1		4.	5
583	CK295	22	0	4	14
3864	CK286	90 1	0	4	13
9747	CK297	53 1		4	12
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ALIGNMENTS

CNS005NG

Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR12G04 of RPCI-98 library from Drosophila melanogaster (fruit
fly) genomic survey sequence.

AL060428.1 GI:4943359

MRDS
GSS.

AL060428.1 GI:4943359

MRDS
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Drosophila melanogaster (fruit fly)
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MENT
Genoscope.

Direct Submission
Direct Submission
Direct Submitted (02-7UN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and haaron Mammoser in Pieter de Jong's laboratory in the Department of

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15721

GGCTCCACTGCTGGGGAAGAGGCCTCTGAAGCAGCAGGACCATCTGCTGTGCCGTGTGTA 15780 CGCAGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACA

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RESULT 14

US-10-796-280-12378

J. Sequence 12378, Application US/10796280

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL510

FILE REFERENCE: CLOOL510

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                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: 6858297 US-10-767-701-27384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27384, Application US/10767701

GENERAL INFORMATION:
APPLICANT: KOVALIC, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5355)B
CURRENT APPLICATION UNMERR: US/10/767,701
CURRENT APPLICATION TOWNERR: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 27384
LENGTH: 490
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CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 68533
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12378
LENGTH: 234309
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Best Local Similarity 52.5%;
Matches 62; Conservative
                                                                                                                                                                 Query Match 8.7%;
Best Local Similarity 51.2%;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 TAACCTTTGGTCTCATTGCCGTTGCGATTACAGTGGTGGCGCATCTTCTTGGCGGTCGAC 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 GIGGIGGCGCAICITCITGGCG 259
282
                                                                            192 AGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTGGTGGCGCATCT 251
AGGTGTTACCAGTGTAGCAGTTGGTGGTAGCTGCCAGAGGCAGCGGAGTGGAGCCAGCGCC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCACCTCAGGCCTCTTTAAGCCTGAAGAAGCGTGGGCCCTACATCTGCTTTTAGTTTTCA 62097
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                                                                                                                                                            Score 28.2; DI
Pred. No. 5.8;
0; Mismatches
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Pred. No. 81;
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Search completed: April 17, 2004, 20:13:04 Job time : 39.4407 secs
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FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605A
CURRENT FILING DATE: 2002-03-27
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2001-01-14
NUMBER OF SEO ID NOS: 361
SOPTWARE: PALENCTH: 8577
TYPE: NUMBER: DATE: 201
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                                                                                                                                         RESULT 11

US-10-796-280-12417/c
US-10-796-280-12417, Application US/10796280

; Sequence 12417, Application US/10796280

; GENERAL INFORMATION: Michele et al.
APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF, FILE REFERENCE: CL001510

; CURRENT APPLICATION NUMBER: US/10/796,280
; CURRENT EILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12417
; ELEGTH: 20618
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; ORGANISM: Drosophila melanogaster
US-10-108-605A-248
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US-10-108-605A-248/c
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                                                                                         US-10-796-280-12417
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Best Local S
Matches 47
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GENERAL INFORMATION:
APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
          Query Match 8.8%;
Best Local Similarity 51.6%;
Matches 65; Conservative
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APPLICANT: Kamdar, Kim
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
                                                                                                          ORGANISM: Homo sapiens
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; Pred. No. 18;
O; Mismatches
            ; Score 28.4; D; Pred. No. 27; 0; Mismatches
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001510
CURRENT APPLICATION NUMBER: US/10/796,280
CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 68533
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12452
LENGTH: 69359
TYPE: DNA
TYPE: DNA
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US-10-796-280-12418
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US-10-796-280-12452
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US-10-796-280-12452
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APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1510

CURRENT APPLICATION NUMBER: US/10/796,280

CURRENT APPLICATION NUMBER: US/10/796,280

CURRENT FILING DATE: 2004-03-10

NUMBER OF SEQ ID NOS: 68533

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12418

LENGTH: 46075
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Matches
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                                                                           Matches
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Best Local &
                                                                                           Query Match

Best Local Similarity 50.0%;
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15661 ĠĠĊĀĀĀGTĠĠĠĠĀTTĀĠĀĀĀCTĀGĠĊĀGTTTGĀCTCCĀGĀGTCTĠTGĊCCCTGTCCĀCTT 15720
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                                   118
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                                   GGCAAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTT
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                                                                           Conservative
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Pred. No. 39;
0; Mismatches
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                                                                         Score 28.4; Di
Pred. No. 47;
0; Mismatches
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US-10-650-609-1/c
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US-10-451-467A-545
                                                                                                                                                      FILE REFERENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10/451,467A
CURRENT FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: EP 00870318.3
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: EP 01870002.1
PRIOR APPLICATION NUMBER: EP 01870003.9
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: EP 01870003.9
PRIOR FILING DATE: 2001-01-09
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 545, Application US/10451467A GENERAL INFORMATION:
                                                                                   SOFTWARE: Pat
SEQ ID NO 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/406582
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 60/426068
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 3
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APPLICANT: Major, Michael
TITLE OF INVENTION: METHODS OF TREATING AGE-RELATED DEFECTS AND DISEASES
FILE REFERENCE: 02-1040-A
CURRENT APPLICATION NUMBER: US/10/650,609
CURRENT FILING DATE: 2003-08-28
CURRENT FILING DATE: 2003-08-28
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEKMANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION
TITLE OF INVENTION: YEAST AND FUNGI
                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CONTRERAS, ROLAND HENRI
APPLICANT: EBERHARDT, INES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                 TYPE: DNA ORGANISM: Candida albicans
                                                                ENGTH: 3042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1109 GAGCTCTGGATTCGGTCGTTTCTGCTGCTTAAACACCTGGTCCAATGTCAAGTAGCGGTT 1050
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                                                                                                              PatentIn
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Krupczak-Hollis,
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is, Katherine
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Pred. No. 9.
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US-10-767-701-21673/c

; Sequence 21673, Application US/10767701

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US04-02000-767/c; Sequence 767, Application PC/TUS0402000; GENERAL INFORMATION:
                                                                                    PCT-US04-02000-767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REPERINCE: 38-21(5355)8
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 21673
LENGTH: 312
TYPE- N.312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.8%;
Best Local Similarity 53.6%;
Matches 59; Conservation
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Best Local
                                                                                                                                            SOFTWARE: PatentIn version 3.2
SEQ ID NO 767
LENGTH: 500
Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                         TITLE OF INVENTION: Method and System for Identifying Biological Entities
TITLE OF INVENTION: Biological and Environmental Samples
FILE REFERENCE: 36609-133264 (SAICTORST-PCT)
CURRENT APPLICATION NUMBER: PCT/US04/02000
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US 60/441,745
PRIOR FILING DATE: 2003-01-23
PRIOR APPLICATION NUMBER: US 60/441,806
PRIOR PILING DATE: 2003-01-23
PRIOR PILING DATE: 2003-01-23
PRIOR PILING DATE: 2003-01-23
PRIOR FILING DATE: 2003-01-23
NUMBER OF SEQ ID NOS: 3242
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ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                         TYPE: DNA
ORGANISM: Escherichia
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  8.8%;
ilarity 50.7%;
Conservative
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; Score 28.4; D; Pred. No. 4.9; O; Mismatches
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Pred. No. 9.
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Pred. No. 4;
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                                        DB 1; Length 500;
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US-10-767-471-10749/c
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; ORGANISM: human metapneumovirus
US-10-789-400-36
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: HEUMATOID ARTHRITIS, METHODS OF DETECTION
ETTE DETERMINE TO TAKE THE DETERMINE ASSOCIATED WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOPTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 10749
LENGTH: 35895
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                                                                                                                                                   Query Match
Best Local Similarity
Matches 65; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Murphy, Brian R.
TITLE OF INVENTION: RECOMBINANT HUMAN METAPNEUMOVIRUS
FILE REFERENCE: 4239-67783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                  FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (1)...(35895)
OTHER INFORMATION: n = A,T,C or G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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les 79; Conserv
           12662
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           GCCTCTCACCCACTGCTCTTGGGTTTGTCTTGGCAGCAAGAGCCCATCCTGGCTG 12603
                                                                             GACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTGGTGGCGCATCTTCTTGGCGG
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Biacchesi, Ster...
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                                                                                                                                                   Conservative
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                                                                                                                                                   Score 30.2; DB Pred. No. 8.2; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30.4; Di
Pred. No. 4.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                      or insertion/deletion polymorphism (see Tables
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밁
                                                                                                                                                                                                                                                             NAME/KEY: misc_feature; LOCATION: (1)...(158027); LOCATION: (1)...(158027); OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism US-10-767-471-10669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-767-471-10669/c
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5355)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 5423
LENGTH: 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10669, Application US/10767471
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUWATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: CL001505
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ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID:
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                                                               48 AGTCATTACTTTTGCGCTCCGGGCGGTTCCGTTCTTAATCCTTAAGCCCCTACGTGAATC
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Similarity 54.0%;
54; Conservative
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Pred. No. 50;
2; Mismatches
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Title:
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Maximum Match 100%
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Maximum DB
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27
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(without alignments)
5694.647 Million cell updates/sec
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| Cgm2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
| Cgm2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
| Cgm2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
| Cgm2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
| Cgm2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
| Cgm2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
| Cgm2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
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8.9 158027

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             US-10-108-605A-248
US-10-796-280-12418
US-10-796-280-12418
US-10-796-280-12378
US-10-796-280-12378
US-10-767-701-25301
PCT-US03-38500-1
US-10-767-701-25301
PCT-US03-38500-1
US-10-767-701-2761
US-10-767-701-2761
US-10-767-701-29783
US-10-100-683-1036
PCT-US04-08299-18
PCT-US04-08299-18
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US-10-789-400-36
US-10-767-471-10749
US-10-767-701-5423
US-10-767-471-10669
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US-10-451-467A-545
US-10-767-701-21673
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Sequence 716, App Sequence 10749, A Pp Sequence 10749, App Sequence 1069, Appli Sequence 1. Appli Sequence 1. Appli Sequence 248, App Sequence 248, App Sequence 12417, A Sequence 12417, A Sequence 12452, A Sequence 2738, A Sequence 2738, A Sequence 2738, A Sequence 1222, A Sequence 1222, A Sequence 2731, Appli Sequence 4460, Ap Sequence 4460, Ap Sequence 4460, Ap Sequence 4460, Ap Sequence 4460, Ap Sequence 1036, Ap Sequence 1353, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl
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8.4	8.4	8.4		8.4	8.4	8.5	8.5	8.5	B.5	8.5	8.5	8. 5	8.5	8.5	8.5	æ.5	8.5	8.6
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PCT-US04-09323-40	US-10-417-884A-1659	US-60-545-213-4448	US-60-545-213-4447	US-60-545-213-176	US-60-545-213-175	US-10-765-790-27	US-10-100-683-5402	US-10-771-241-144	US-10-767-701-12271	US-10-767-701-18755	US-10-796-307-8720	US-10-796-280-12200	US-10-796-280-12303	US-10-767-701-29976	US-10-796-307-18171	US-10-767-471-27441	US-10-767-471-27293	US-10-100-683-3274
Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
40, Appl	1659, Ap	4448, Ap			175, App	27, Appl	N 1		12271, A	Ç	8720, Ap	12200, A	12303, A	29976, A	•	~	•	3274, Ap

ALIGNMENTS

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Sequence 716, Application US/10021698A

Sequence 716, Application

APPLICANT: KEITH, TIM

APPLICANT: LITTLE, RANDALL

APPLICANT: VAN EERDEWEGH, PAUL

APPLICANT: UPOUTS, JOSEE

APPLICANT: DL MASTRO, RICHARD

APPLICANT: BLE MASTRO, RICHARD

APPLICANT: SIMON, JASON

APPLICANT: ALLEN, KRISTINA

APPLICANT: HANDIT, SUNIL

ITTLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES RELATING TO

ITTLE OF INVENTION: RESPIRATORY DISEASES AND OBESITY

ITTLE REFERENCE: 2976-4044US1

CURRENT APPLICATION NUMBER: 05/211,749

PRIOR APPLICATION DATE: 2001-10-22

PRIOR APPLICATION NUMBER: 60/211,749

PRIOR PILING DATE: 2000-06-14

INUMBER OF SEQ ID NOS: 6160

SOPTWARE: Patentin 2.1

SEQ ID NO 716

LENGTH: 173233

TYPE: DNA
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                                                                                                                                                          Query Match
Best Local S
Matches 65
                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified base
LOCATION: (88987). (89986)
OTHER INFORMATION: a, t, c or
FEATURE:
NAME/KEY: modified base
LOCATION: (167286)...(167385)
OTHER INFORMATION: a, t, c or
84548
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                                      260
                                                                                                             200 AGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTGGTGGCGCATCTTCTTGGCG
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l Similarity 55.1%;
65; Conservative
GTAACTCCAACCCTCTGCTCGTTGGCCTTGTCACCTCAGTGCTGATTTTGCAGATGAA 84605
                                    grosacscaccrostreaccerrescerescaccarcerrrrsgresacrescaa, 317
                                                                               AGAATCTAAGCCTTGACCAAATATGTGTTACTATTACTTTTGTTGTTGTTGTTGTTCTGG 84547
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RESULT 2

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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEB: No. 603115018
STEET: Ope Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
COUNTY: Philadelphia
STATE: PA
COUNTY: Philadelphia
STATE: PA
COUNTY: Philadelphia
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPS/MS-DOS
SOPTHARE: Patentin Release #1.0, Version #1.25
CORRENT APPLICATION NUMBER: US/08/476,900A
FILING DATE: 0-JUN-1995
CILASSIFICATION NUMBER: US/08/476,900A
FILING DATE: 10-TUN-1995
FILING DATE: 34.293
REFERENCE/DOCKET NUMBER: BYLK-0027
THLEPOLOMINICATION INFORMATION:
NAME: Beardell, Lori Y.
REFERENCE/DOCKET NUMBER: BYLK-0027
THLEPOLOMINICATION INFORMATION:
NAME: Beardell, Lori Y.
REFERENCE/DOCKET NUMBER: BYLK-0027
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US-08-404-531B-4/c
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                                                                                                                                                                                                                                   TELEPAX: 215-500 IN NO: 4:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5110 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                      US-08-404-531B-4
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best Local Similarity 58.4%;
Matches 52; Conservarion
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GENERAL INFORMATION:
                                                                                                                           Matches
                                                                                                                                        Query Match
Best Local (
                                                                                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 586372471s
STREET: One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3965
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                                                                                          118 GGCAAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTT 177
                                                                                                                         Similarity
52; Conser
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   CGGAAAAAGGCGAGAGAGAAGGAGGATTT 4412
                              CGCAGCAATGCGATAGATCTGAAGACTCT
                                                             GGCAGCTTGGCGATGTCAATGCCATCGATGATGATACGCCCTTCAAACATATCCACCATT 4441
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Thomas, Gilbert Cote, and Robert Gagel
                                                                                                                           Conservative
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                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                        9.2%;
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Pred. No. 2.
                                                                                                                           Pred. No. 3;
0; Mismatches
                                                                                                                                        Score 29.8;
Pred. No. 3;
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                                                                                                                                                         Length 5110;
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Sequence 4, Application US/08476900A
Patent No. 6031150
GENERAL INFORMATION:
APPLICANT: JOSEPH Bryan, Lydia Agu
TITLE OF INVENTION: Sequence Encod
Patent No. 6031150
TITLE OF INVENTION: and Method of
TITLE OF INVENTION: Infancy
NUMBER OF SEQUENCES: 49
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US-08-476-900A-4/c
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NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,531B
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, APPLICANT: Thomas, Gilbert Cote, and Robert Cagel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 5863724ris
STREET: One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 5110 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Encoding Mammalian Sulfonylurea Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 5110;
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CORRESPONDENCE

ADDRESS:

and Method of Detecting Persistent Hyperinsulinemic Hypoglycen

yan, Lydia Aguilar Bryan, Daniel Nelson Sequence Encoding Mammalian Sulfonylure

Sulfonylurea Receptor

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US-08-476-900A-27/c
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; LOCATION:
US-08-404-531B-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6031150
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                     TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 4635 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                      NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BY.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                           CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,900A
FILING DATE: 07-UN-1995
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: COMPUTER: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Da
TITLE OF INVENTION: Sequence Encoding Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
FRAGMENT TYPE:
                                                    SEQUENCE CHARACTERISTICS:
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YPOTHETICAL: NO
NTI-SENSE: NO
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CITY: Philadelphia
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                   ENGTH:
TRANDEDNESS:
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o. 6031150
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             nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                          One Liberty Place 46th. Floor
                                 4635 base pairs
                                                                                                                                                                                                                                                                                                                                                                                       USA
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an Sulfonylurea Receptor
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                       TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                      CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,546A
FILING DATE: 07-UNE-1995
CLASSIFICATION: 800
                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 4635 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                 HYPOTHETICAL:
                                               MOLECULE TYPE:
RAGMENT TYPE: N-terminal
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LOCATION:
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nes 52; Conserv
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 15-MAI
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CITY: Philadelphia
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ADDRESSEE: No. 6054313ris
STREET: One Liberty Place 46th. Floor
                                                                     TOPOLOGY: lir
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                                                                                                                                                                                         CELEPHONE:
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                                                                                                    nucleic acid
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Thomas, Gilbert Cote, and Robert Gagel
VENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
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                                                                                                                                                           27:
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Pred. No. 2
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LOCATION: NAME/KEY:

CDS 37..4533

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APPLICANT: KESHI ET AL
TITLE OF INVENTION: PROBE FOR DIAGNOSING INFECTIOUS DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08809254A Patent No. 6660852
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Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 56703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 19036/33767
CURRENT APPLICATION NUMBER: US/08/809,254A
CURRENT FILING DATE: 1997-05-16
PRIOR APPLICATION NUMBER: PCT/JP95/02036
PRIOR FILING DATE: 1995-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQ ID NO 4
LENGTH: 5829
TYPE: DNA
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APPLICANT: DORNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial sequence
                                            FILING DATE:
APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
COPPRAPING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463
                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
FITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OR APPLICATION NUMBER: JP 236348
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                              CITY: Alexandria
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ilarity 57.1%;
Conservative
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               Stephen A.
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                                                                                        EP 91 114 300.6
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30472/114 IMMU
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US-08-404-531B-27/c
US-08-404-531B-27/c
I Sequence 27, Application US/08404531B
Fatent No. 5863724
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL THOMAS, Gilbert Cote,
APPLICANT: Thomas, Gilbert Cote,
APPLICANT: Thomas, Gilbert Cote,
APPLICANT: Thomas, Gilbert Cote,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: (703)836-9300
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 9.4%; Score 30.6;
Local Similarity 1.0%; Pred. No. 1.9
les 3; Conservative 179; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                             STREET: One ____
CITY: Philadelphia
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NAME: Beardell, Lor
REGISTRATION NUMBER:
                                                  CLASSIFICATION:
                                                                                                                                                                                                             COUNTRY: U
                                                                                                                                                                                                                                                                             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 5863724ris
STREET: One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                    APPLICATION NUMBER: US/08/404,531B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 CTGGTGAATCTTTTC 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 GCGGTTCCGTTCTTAATCCTTAAGCCCCTACGTGAATCACAATTTGTGGGCAAAATGGCG 129
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DEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                  Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson,
Thomas, Gilbert Cote, and Robert Gagel
ENTION: Sequence Encoding Mammalian Sulfonylurea
                                                                                                                                                                                                                            USA
                                                                   15-MAR-1995
                                                                                                                                                                                                                                                                                                                                                    49
34,293
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                                                                                                                       Version
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US-09-328-352-1339
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US-09-252-991A-13832/c
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13729
LENGTH: 594
                               Sequence 1339, Application US/09328352

Patent No. 6562958

Patent No. 6562958

PRICAMIC SEQUENCES AND SEQUENCES RELATING TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: BADWANNII FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 1339

LENGTH: 1404
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SEQ ID NO 13832
LENGTH: 678
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Best Local
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
)9-252-991A-13832
ORGANISM: Acinetobacter baumannii
                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407 TATAGGCCTTGCCCTCGTCGGGGTTGAAGTCGCCGTGGCGGCGCTTGATCTTGCTGATCC 348
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Pred. No. 0.025;
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                                                                                                                                                                                                                                                                                                                        NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 9834
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 2387 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charles I
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER; HP Vectra
OPERATING SYSTEM: MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                           9.7%;
Local Similarity 52.7%;
Les 68; Conservative
1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 ATTCCAATGGGAGTATTGGGCATATTAATGACATTAAAGGTCATGCCAAATGTAAAAGAG
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61; Conserva
                             232
                                                                                                                                962
                                                                                                172 ACGTTTCGCAGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCG 231
                                                                                                                                                             112 TTTGTGGGCAAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCA 171
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                                                               GCAATTCAACGGTATTCTCCAAATGAGAAAATTCAAACAGTTAGTCCTTCTGCCTTAAAT 1081
ATGATTGTG 1090
                               ATTACAGTG 240
                                                                                                                                Maryland
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                                                                                                                                                                                               Score 31.4; DB Pred. No. 0.51; 0; Mismatches
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APPLICANT: EGGELING, LOTHAR
APPLICANT: PREFFERLE, WALTER
ITITLE OF INVENTION: NUCLECTIDE SEQUENCE CODING FOR THE EXPORT OF
ITITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
ITITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
ITITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
ITITLE REFERENCE: 21123/265496/MAS
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO1
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Patent No. 6613545
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NAME/KEY: gene
LOCATION: (101).. (853)
OTHER INFORMATION: brnF
NAME/KEY: gene
LOCATION: (853).. (1176)
OTHER INFORMATION: brnE
OTHER INFORMATION: ATCC14752
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APPLICANT: KENNERKNECHT, NICOLE
APPLICANT: SAHM, HERMANN
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RESULT 3 US-09-471-803A-6

QUENCES RELATING TO PSEUDOMONAS THERAPEUTICS

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APPLICANT: KENNERKNECHT, NICOLE
APPLICANT: SAHM, HERMANN
APPLICANT: SAHM, HERMANN
APPLICANT: SAHM, HERMANN
APPLICANT: PFEFERLE, WALTER
APPLICANT: PFEFERLE, WALTER
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: ERANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/265496/MAS
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
US-09-252-991A-13729/c

Sequence 13729, Application US/09252991A

Patent NO. 655179; Application US/09252991A

Patent NO. 655179; Application US/09252991A

PAPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPE

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPE

TILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18
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; LOCATION: (853)..(1176)
; OTHER INFORMATION: brnE
; OTHER INFORMATION: ATCC13032
US-09-471-803A-6
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ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: gene
LOCATION: (101)..(853)
OTHER INFORMATION: brnF
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US-08-444-531B-5
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US-09-205-258-173	US-08-671-548C-7	US-09-198-452A-1	US-09-610-040-5	US-09-194-036B-74	US-08,-651-155B-74	US-09-453-702B-174	US-08-387-942C-35	US-09-621-976-15639	US-08-961-527-41	US-09-216-393B-345	US-09-216-393B-343	US-09-216-393B-342	US-09-216-393B-340	US-08-387-942C-1	US-09-976-594-152	US-09-208-716-2	US-08-726-320-2
Sequence :	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	sequence
7	7, Appli	۲	5, Appli	74, Appl	74, Appl	174, App	35, Appl	15639, A	41, Appl	345, App	•	342, App	340, App	1, Appli	152, App	2, Appli	2, Appli

ALIGNMENTS

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APPLICANT: SAMM, HERMANN
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
APPLICANT: EFFFERLE, WALTER
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/265496/MAS
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT FALING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 4
LENGTH: 324
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (1). (124)
COTHER INFORMATION: 571E
                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: brnE
OTHER INFORMATION: ATCC14752
US-09-471-803A-4
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US-09-471-803A-4
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GENERAL INFORMATION:
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Best Local Similarity
Matches 324; Conservat
181
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                         AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTG
                                                                                                             AAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTTCGC
                                                                                                                                                                   GCGCTCCGGGCGGTTCCTTAATCCTTAAGCCCCTACGTGAATCACAATTTGTGGGC
AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTTGCGGATTACAGTG
                                                                                    AMANTGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTTCGC
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                                                                                                                                                                                                                                                                                                                                                                                Length 324;
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Search completed: April 19, 2004, 11:42:06 Job time : 151.886 secs
                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 9.9%; Score 32; DB 8; Length 470; Best Local Similarity 51.9%; Pred. No. 2.2; Matches 68; Conservative 0; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to oligonucleotide clones originating in barley (Hordeum vulgare) which contain single nucleotide polymorphisms (SNP). The oligonucleotides may be used for analysis of SNPs among barley varieties, identification of particular varieties and genotype-phenotype analysis, isolation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties. The present sequence represents an oligonucleotide clone DNA sequence featured in the specification. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published-pct-sequences. (Updated on 27-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 470 BP; 122 A; 131 C; 102 G; 106 T; 0 U; 9 Other;
                                                                                                                                                       301
                                                                                                                                                                                                             324
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                                                                                                     264 TGGGTGAGCCT 254
                                                                                                                                                                                                                                                    241 GTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTT 300
                                                                                                                                                                                                                                                                                                                  384 ATCAAGNACAGGGAGNAGCATAAGGGAACCTTTGAGNCCATCCACGTTGAGGATGCCCAG 325
                                                                                                                                                     TTTGTTGGACT 311
                                                                                                                                                                                                          GGTCACCAGTTTGCCACCCGTCTGGGCAACGTGTTCACCATTGGCAAGGGCACCAAGCCT 265
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RESULT 14
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20-DEC-2001;
20-DEC-2001;
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20-DEC-2001;
27-SEP-2002;
                                    Single nucleotide polymorphism sites in barley varieties and DNA sequences containing them for analysis and identification of barley varieties and production of barley transformants with desired
                                                                                                                                                                                                           WPI; 2003-587127/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA clone originating in barley containing SNP encoding sequence
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characteristics.
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Pred. No. 1
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Disclosure; SEQ ID

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Disclosure; SEQ ID XX; 284pp; Japanese

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-2001;
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17-OCT-2003
                                                                                                Single nucleotide polymorphism sites in barley varieties and sequences containing them for analysis and identification of varieties and production of barley transformants with desired
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                                                                          characteristics.
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The present invention describes a compound (I) that is 8-50 nucleobases in length: (a) targets a nucleic acid molecule encoding major histocompatibility complex (MHC) class II transactivator, and specifically hybridises with the nucleic acid encoding the MHC class II transactivator, and inhibits the expression of MHC class II transactivator; or (b) specifically hybridises with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding MHC class II transactivator. (I) has immunosuppressive, antimicrobial, antidiabetic, antirheumatic, antiarthritic, cytostatic, nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; major histocompatibility complex class II transactivator; MMC class II transactivator; antisense modulation; immunosuppressive; antimicrobial; antidiabetic; antixheunatic; antiarthritic; cytostatic; nootropic; neuroprotective; immunostimulant; autoimmune disorder; mMC class II transactivator inhibitor; infection; transactivator inhibitor; infection; transactivator inhibitor; infection; disease; gene; ss. multiple sclerosis; severe combined immunodeficiency disease; gene; ss.
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                                                                                                                                                                                                                                                                                   Example 13; Page 93-99; 129pp; English.
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                                                                                                                                                                                                                                                                                                                                                                    antisense oligonucleotides for modulating MHC class II transactivator expression, particularly useful for treating autoimmune disorders has transplant rejection, Alzheimer's disease, or multiple sclerosis,
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Matches 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6672
                                              Single nucleotide polymorphism sites in barley varieties and DNA sequences containing them for analysis and identification of bar varieties and production of barley transformants with desired
                                                                                                                             Sato
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20-DEC-2001; 2001JP-00387131.
20-DEC-2001; 2001JP-00403299.
20-DEC-2001; 2001JP-00403300.
27-SEP-2002; 2002JP-00327515.
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                                                                                                                                                                                                                                                                                                                                          Hordeum vulgare; var.
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17-0CT-2003
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Disclosure; SEQ ID

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284pp; Japanese

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RESULT 11
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gene therapy;
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prostate; pancreas; carcinoma; antitumour; cancerous;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy; antineoplastic;
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The present invention describes a method (M1) for screening for an anti-
CC neeplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. MI can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. MI can be used in the treatment of cancer such
CC activity and cancer, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
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28-SEP-2000;
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2000US-0237425P.
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Matches 73
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                                                                                                                                                                                                                                                                      21-APR-2000;
02-JUN-2000;
07-JUL-2000;
sequences AAS59506-AAS59804 represent DNA molecules encoding Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
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                                                                                                   Propionibacterium acnes polypeptides and nucleic vaccinating against and diagnosing infections, estreating acne vulgaris.
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                                                                         Claim 1; SEQ ID NO 10; 1069pp; English
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                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
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, Wang S, Jen S,
, Vallieve-Douglass
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lss J;
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Pred. No. 1:
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New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

Claim 1; SEQ ID NO 10; 1481pp; English

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                                                Identifying at least pathogenic infection bacterial, fungal or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant; bacterial infection;
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S, Tao
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                                                one gene involved in plant resistance or response for conferring resistance or tolerance to a plant viral infection by determining or detecting plant
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Pred. No. 2.1
O; Mismatches
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Whitham S, Xie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genomic polynucleotide SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAACTGATTTCTCCTGTATTCTCCTTGTTGTCGCAGTATGTGCAGTCATTACTTTTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | |:: |::| |:::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |::| |:::| |:::| |:::| |:::| |:::| |::| |:::| |:::| |::
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ilarity 12.9%; Pred. No. 0.4
Conservative 105; Mismatches
                                                                                                                                              detection reagent for detecting 1000 for elucidating cell signaling and ce
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NO 32863; 21pp + Sequence Listing;

isolated

nucleic acid

detection

English

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1153 301

TTTGTTGGACTGGTGAATCTTTTC

324 1176

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RESULT
AAH2111
This invention describes a novel isolated polynucleotide (I) containing CC at least one sequence that (i) is 70% identical with a sequence that CC encodes at least one of 251 amino acid (as). (3) or 108 as (5) CC polypeptides, (ii) encodes a polypeptide at least 70% identical with (3) CC or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least CC 15 consecutive bases from (i)-(iii). The invention also describes (a) CC protein derived from sequences of 753 bp (2) or 324 bp (4); (b) CC coryneform microorganisms, especially Covynebacterium, transformed with CC coryneform microorganisms, especially Covynebacterium, transformed with CC coryneform bacteria in which the CC branched-chain I-aa by fermentation of coryneform bacteria in which the CC branched-chain I-aa by fermentation of coryneform bacteria in which the CC specially overexpressed; and (d) method for isolating the brnB and/or CC especially overexpressed; and (d) method for isolating the brnB and/or CC used for fermentative production of branched-chain amino acids, coryneform bacteria being CC sprebacterium; laucine, isoleucine and valine, which are useful in medicine CC and animal nutrition. (I) can also be used as source of primers and probes for isolation of related sequences. Transformation with (I) CC increases yield of branched-chain amino acids. This sequence encodes the CC corynebacterium glutamicum AFCC 13032 brnF and brnB proteins described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-amino acid production; brnF; coryneform bacterium; leucine;
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                                                                                                                                                                                                                                                                                                                                                                           Claim 4 (i); Page 17-18; 23pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                           genes from coryneform bacteria, useful for increasing ve production of branched-chain amino acids.
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853. .1179
/*tag= b
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Seguence

1271

B₽;

265 Ņ

328

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318

<u>ن</u>

360

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from

SEQ

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NO 1; 246pp +

Sequence

Listing;

English.

gene.

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RESULT 6
AAH64
AAH64
AC AAH6
AC AAH6
AC AAH6
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07-APR-2000;
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                                                                                                               Corynebacterium
                                                                                                                                                                                                                  L-amino acid production; brnF; coryneform bacterium; leucine;
                                                                                                                                                                                                                                                                                                                          C. glutamicum
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   Location/Qualifiers 101. .856
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Pred. No. 8.8e-101;
                                                                                                                                                                                                                      isoleucine; valine;
                                                                                                                                                                                                                                                         brnE; branched-chain amino
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This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that (c) encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) cc encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) cc (5); (iii) encodes a polypeptide at least 70% identical with (3) cc (c) (ii); (ii) encodes a polypeptide at least 70% identical with (3) cc (c) (iii) is the complement of (i) or (ii), or (iv) contains at least 15 consecutive bases from (i) (iii). The invention also describes (a) cc (c) protein derived from sequences of 753 bp (2) or 324 bp (4); (b) cc (c) contour microorganisms, especially cyrnebacterium, transformed with (c) one or more (I), where these are replicative DNA; (c) production of coryneform bacteria in which the cc brnE and/or brnF genes (or equivalent sequences) are amplified, cc brnE and/or brnF genes (or equivalent sequences) are amplified, cc especially overexpressed, and (d) method for isolating the brnE and/or brnF genes. (I) is used for transformation of coryneform bacteria being cused for fermentative production of branched-chain amino acids, and animal nutrition. (I) can also be used as source of primers and corynebase for isolation of reaching and sequences encodes the corynebacterium glutamicum, ATCC 14752 brnF and brnE proteins described in corynebacterium glutamicum, ATCC 14752 brnF and brnE proteins described in
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                       Matches 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New export genes from coryneform bacteria, useful for increasing fermentative production of branched-chain amino acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (i); Page 13;
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                                                                                                                                                                                                                         GCGCTCCGGGCGGTTCCTTAATCCTTAAGCCCCTACGTGAATCACAATTTGTGGGC
                                                             AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTTGCGATTACAGTG
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GTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTT
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                                                                                                16-DEC-1999;
07-APR-2000;
03-AUG-2000;
               Nakagawa
Tateishi
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2000JP-00159162.
2000JP-00280988.
               Mizoguchi H, Ando S, Hayashi
Senoh A, Ikeda M, Ozaki A;
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XX DE11
XX DE11-I
ST 13-J

Coryneform; nucleic acid array;

Corynebacterium

glutamicum

13-JUN-2001; 2001DE-01028510.

19-DEC-2002.

C. glutamicum

SEQ ID 1961

fermentation;

culture;

04-JUN-2003 ACA01970;

(first entry) derived ORF

ACA01970 standard; DNA;

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Matches 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 324 BP;
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P-PSDB; AAG90036.
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TTTGTTGGACTGGTGAATCTTTTC 324
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Mismatches 0;
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Gapop 10.0 , Gapext 1.0
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   US-10-608-504-6_COPY_853_1176
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ADB06513
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ACF39600
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Aah62166 C glutami
Ada71938 Rice gene
Ab127130 Drosophil
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1925 DNA clone

1925 DNA clone

1938 DNA clone

1938 DNA clone

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1938 Human cDN

1945 Human cDN

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Acl20924 DNA clone	Acl20907 DNA clone	Acl20947 DNA clone	Ac120906 DNA clone	Acl20912 DNA clone	Ac120920 DNA clone	Acl20954 DNA clone	Acl20950 DNA clone	Acl20929 DNA clone		Abx03452 Negative-	φ	Aca50939 Prokaryot	ω	Aah41227 Pyrococcu	Aat30053 S. pneumo	Abs99007 Enterococ	Aax13212 Enterococ	Aah24065 Yeast AOD	Continuation (8 of	Aav52189 Streptoco	Ada30052 DNA encod

ALIGNMENTS

L-amino acid production; brnF; coryneform bacterium; leucine; animal nutrition; ds. C. glutamicum AAH21111; AAH21111 standard; DNA; 324 BP. EP1096010-A1. Corynebacterium glutamicum. 05-SEP-2001 (first entry) BrnE DNA. brnE; branched-chain amino acid; isoleucine; valine; medicine;

27-OCT-1999; 02-MAY-2001. (DEGS) DEGUSSA AG. (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH. 11-OCT-2000; 2000EP-00122057. 99DE-01051708.

WPI; 2001-391595/42. P-PSDB; AAB86248. Kennerknecht N, Eggeling ŗ Sahm H, Pfefferle

Ξ

New export genes from coryneform bacteria, useful for increasing fermentative production of branched-chain amino acids.

Claim 5; Page 16; 23pp; German.

This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) polypeptides; (ii) encodes a polypeptide at least 70% identical with (3) or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least 15 consecutive bases from (i)-(iii). The invention also describes (a) protein derived from sequences of 753 bp (2) or 324 bp (4); (b) coryneform microorganisms, especially Corynebacterium, transformed with one or more (I), where these are replicative DNA; (c) production of

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (5749. .9069)
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complement (5749. .9069)
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Search completed: April 19, 2004, 18:30:07 Job time : 1375.24 secs
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Best Local Similarity 47.0
Matches 118; Conservative
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'transl_table=11
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Pred. No. 2.4;
0; Mismatches 133; Indels
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DEFINITION
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Best Local Simi
Matches 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum Corynebacterium glutamicum Gorynebacterium glutamicum Bacteria; Actinobacteria; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                           Campylobacter fetus
Campylobacter fetus
                                                                                                                                                                                                     AY211269 65865 bp
Campyloacter fetus strain 23D 8
AY211269 AF027405 J05577 L15800
AY211269.1 GI:28974206
2 (bases 1 to 65865)
Blaser,M.J. and Gotschlich,E.C.
Surface array protein of Campylobacter fetus. Cloning and
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                                                                                            Surface array
                                                                                                          Blaser, M.J. and Gotschlich, E.C.
                                                                                                                    Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacteraceae, Campylobacter.

1 (bases 1 to 65865)
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HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
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5 AX114121
5.1 GI:140
                                                                   Chem.
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/db_xref="taxon:1718"

/note="seq 1 to long (3.309.400)

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Pred. No. 1.1e-88;
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    Hayashi, M., Ochiai
    Ikeda, M. and Ozaki, A.

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91035477
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Thompson, S.A., Shedd, O.L., Ray,
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note="Cf0001"
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                                                                                                          serotype="A"
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Submitted (30-SEP-1997) Division of Infectious Dis University, A-3310 MCN, Nashville, TN 37232, USA 10 (bases 1 to 65865) Th.Z.-C., Wassenaar, T.M., Thompson, S.A. and Blaser Direct Submission
Submitted (03-JAN-2003) Microbiology and Medicine, University School of Medicine, VAMC ROOM 6006W 423 New York, NY 10016, USA On or before Mar 15, 2003 this sequence version regi:4009445, gi:144211, gi:289533, gi:913763.
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Dworkin, J., Tummuru, M.K. and Blaser, M.J.

A lipopolysaccharide-binding domain of the Campylobacter fetus S-layer protein resides within the conserved N terminus of a fa of silent and divergent homologs

J. Bacteriol. 177 (7), 1734-1741 (1995)
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Tummuru, M.K. and Blaser, M.J.
Tummuru, M.K. and Blaser, M.J.
Rearrangement of sapA homologs with conserved and in Campylobacter fetus
Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7265-7269 (
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Tummuru,M.K. and Blaser,M.J.
Characterization of the Campylobacter fetus sapA
that the sapA promoter is deleted in spontaneous
J. Bacteriol. 174 (18), 5916-5922 (1992)
                                                                                                                                                                                                                                                                                                                                                                                 Division of Infectious Diseases,
dicine, Nashville, TN 37232, USA
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PF001751:Toprim domain
PF02518:Histidine kinase-, DNA gyrase B-, phytochrome-like
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gene CDS

gene Sg

DNA

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PAT 11-MAY-2001

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Query Match
Best Local S
Matches 324
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                                                                                                                                                 Corynebacterium glutamicum ATCC 13032
Corynebacterium glutamicum ATCC 13032
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP005274 340000 bp DNA Corynebacterium glutamicum ATCC 13032 DNA,
Unpublished
                                                                          Nakagawa, S.
                                                                                                                                                                                                                                                                                                                                                     AP005274.1
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                                     Complete genomic sequence of Corynebacterium glutamicum ATCC 13032
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AUTHORS
TITLE
JOURNAL
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This sequence is conducted by collaboration of Kyowa Hakko Kogyo Co. Ltd. And Kitasato University.
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Direct Submission
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SMEIVQNGINLAATDXFRLATATTALLDNARSLDSGLNDS
SMEIVQNGINLAATDXFRLATATTALLDNARSLDSGLNDS
SMEIVQNGINLAATDXFRLATATTALLDNARSLDSGLNDS
SMEIVQNGINLAATDXFRLATATTALLDNARSLTTALLDNARSLDSGLNDS
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/notee="PF00308:Bacterial dnaA protein
TIGR00362:DnaA: chromosomal replication initiator protein
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/gene="Cg10002"
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                                                                          DAIRRVSLVAERNAQIVLHFSEGQVILTAGATEAGHAEETLPCAFTGKELTIAFNPGY
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                                         LKDGLSVVPTSRAVFGFTEPSRPAIMIPEPEEMPSANENGIFQTPDTYFTYLLMPVRI
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/gene="Cgl0003"
/EC_number="2.7.7.7"
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/strain="ATCC 13032"
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/transl_table=
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RESULT 13 AP005274

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Query Match 100.0%; Score 324; DB 6; Best Local Similarity 100.0%; Pred. No. 5.8e-89; Matches 324; Conservative 0; Mismatches 0;
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Kennerukunehito,N., Sahm,H., Eggering,L. and Pfefferle,W.

Kennerukunehito,N., Sahm,H., Eggering,L. and Pfefferle,W.

Nucleotide sequence encoding the discharge of branched amino acio
method of isolating the same and utilization thereof

Patent: Up 200169788-A 4 26-UNI-2001;

DEGUSSA HUELS AG, FORSCHUNGSZENTRUM, UDELICH GMBH

OS Corynebacterium glutamicum ATCC13032

Up 2001169788-A/4

PD 26-UNI-2001

PD 26-UNI-2001

PF 24-OCT-2000 UP 2000324315

PF 24-OCT-1999 DE 19951708-8

PI NICOLE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, WALTER

PFEBFERLE

DEGUSSA GENERALING GENERALING SAHM, LOTHAR EGGERING, WALTER
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Nucleotide sequence encoding method of isolating the same BD014994

BD014994.1 GI:22555801
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                                                                                                                                                                                                                                                                                                                                                                                NICOLE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, WALTER
                                                                                          /organism="unidentified"
/mol_type="genomic DNA"
/db_xref≈"taxon:32644"
                                                                                                                                                                   Location/Qualifiers
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the discharge of branched amino acid,
and utilization thereof.
                                     Length 1271;
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Corynebacterineae; Corynebacteriaceae; Corynebacterium.

I (bases 1 to 2105)

Kennerknecht, N., Sahm, H., Yen, M.R., Patek, M., Saier Jr, M.H.
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Corynebacterium glutamicum BrnE (brn
regulator (lrp) genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Kennerknecht,N., Eggeling,L. and Sahm,H.
Direct Submission
Submitted (07-NOV-2001) IBT-1, Forschungszentrum, Leo-Brandt Str.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eggeling,L.

Export of L-isoleucine from Corynebacterium glutamicum:
two-gene-encoded member of a new translocator family
J. Bacteriol. 184 (14), 3947-3956 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                       Juelich
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                                                                                                                                                                                                                                                                                                     /organism="Corynebacterium
/mol_type="genomic DNA"
/db_xref="taxon:1718"
complement(385. .711)
                                                           GLVNLF"
                                     complement (708. .1463)
                                                                          /trānslation="mttdfsCillvvavCavItfalravpflIlkplresQfvGkmam
wmpaGILaIltastfrsnaIdlktltfgLIavaItvvAhllGgrrtllsvGagTIvfv
                                                                                                                                                                                                        acid export protein"
                                                                                                                                                                                                                                                                  complement (385. .711)
    complement (708. .1463)
                                                                                                             /protein_id="AAM46685.1"
/db_xref="GI:21311380"
                                                                                                                                                    /product="BrnE"
                                                                                                                                                                   transl_table=11
                                                                                                                                                                                                                             note="LIV-E transporter component 1; branched-chain amino/
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Degussa AG (DE) ; FORSCHUNGZENTRUM JUELICH GMBH (DE)
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PI NICOLE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, WALTER PI	
27-OCT-1999 DE 19951708.8	
24-OCT-2000	
PD 26-JUN-2001	
OS Corynebacterium glutamicum ATCC14752	COMMENT
DEGUSSA HUELS AG, FORSCHUNGSZENTRUM JUELICH GMBH	
Patent: JP 2001169788-A 1 26-JUN-2001;	JOURNAL
method of isolating the same and utilization thereof	
Nucleotide sequence encoding the discharge of branched amino acto,	TITLE
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1 (bases 1 to 1271)	REFERENCE
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Kennerknecht, N., Sahm, H.,
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Kennerknecht, N., Sahm, H., Eggeling, L. and Pfefferle, W.
Nucleotide sequences coding for the export of branched chain
acids, process for the isolation thereof and use thereof
Patent: US 6613545-A 6 02-SEP-2003;
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AX137709
AX137709.1
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Degussa AG (DE); FORSCHUNGSZENTRUM JUELICH GMBH Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="ATCC14752"
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from Patent EP1096010.
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E (Dases 1 to 324)

Kennerukunehito,N., Sahm,H., Eggering,L. and Pfefferle,W.

Nucleotide sequence encoding the discharge of branched amimethod of isolating the same and utilization thereof

Patent: JP 2001169788-A 3 26-UNH-2001;

DEGUSSA HUELS AG,FORSCHUNGSZENTRUM, JUELICH GMBH

OS COTYNEBACTERIUM GILLEMICUM ATCC14752

PN JP 2001169788-A/3

PD 24-OCT-2000 JP 2000324315

PP 24-OCT-2000 JP 2000324315

PP 24-OCT-1999 DE 19951708.8

PI NICOLE KENNERUKUNEHITO,HERMANN SAHM,LOTHAR EGGERING,W

PPEFFERLE

PC C12N15/09,C12R1:15),(C12N1/21,C12P13/06,C12P

PC (C12N15/09,C12R1:15)

PC (C12N15/00,C12R1:15)

PC (C12N15/00,C12R1:15)

FT CDS

Location/Qualifiers

FT CDS

FT CDS

Location/Qualifiers
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BD014993.1 GI:22555800
JP 2001169788-A/3.
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                                                                                                                                                                  AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTG
                                                                                                                                                                                                           AAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTTCGC
                                                                                                                                                                                                                                     AAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTTCGC
                                                                                                                                                                                                                                                                                  GCGCTCCGGGCGGTTCCGTTCTTAATCCTTAAGCCCCTACGTGAATCACAATTTGTGGGC
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                                   TTTGTTGGACTGGTGAATCTTTTC 324
                                                                                 GTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTT
              TTTGTTGGACTGGTGAATCTTTTC 324
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24-OCT-2000 JP 2000324315
27-OCT-1999 DE 19951708.8
NICOLE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, WALTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C12N15/09, C07K14/34, C12N1/21, C12P13/06, C12P13/06, C12P13/08// (C12N15/09, C12R1:15), (C12N1/21, C12R1:15), (C12P13/06, C12R1:15) C12N15/00,
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DEFINITION
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AUTHORS
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DE C12N15/09,C12N15/09,C07K14/34,C07K16/12,C07K16/40,C12M1/00, PC

C12N1/19,C12N15/09,C07K14/34,C07K16/12,C07K16/40,C12M1/00, PC

C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12N9/02,C12P7/40,C12P13/PC

C12P13/08,
PC C12P19/00,C12P19/34,C12P21/02,C12Q1/37,C12Q1/68,G01N33/53, PC

G01N33/566,G01N33/68,G01N37/00//C12P21/08,(C12N1/21,C12P1

PC G12N15/00,C12N15/00
PC C12N5/00,C12N15/00
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Nakagawa,S., Mizoguchi,H., Ando,S., Hayash
Yokoi,H., Tateisichi,N., Senoo,A., Ikeda,M.,
Novel polynucleotide
Patent: JP 2002191370-A 290 09-JUL-2002;
KYOWA HAKKO KOGYO CO LTD
OS Corynebacterium glutamicum
PN JP 2002191370-A/290
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KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
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Corynebacterium glutamicum
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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Degussa AG (DE) ; FORSCHUNGSZENTRUM JUELICH GMBH (DE)
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Sequence 4 from Patent EP1096010.
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/db_xref="taxon:1718"
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nucleic search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

Minimum DB Maximum DB

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Listing first 45 summaries
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1 (bases 1 to 324)

1 (bases 1 to 324)

Kennerknecht,N., Sahm,H., Eggeling,L. and Pfefferle,W.

Kennerknechtde sequences coding for the export of branched chain amino acids, process for the isolation thereof and use thereof patent: US 6613545-A 4 02-SEP-2003;
                                                                                                                                                                                AR391955
Sequence 4 from patent US
AR391955
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BE013856.1 GI:8274843
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1 (Dases 1 to 539)
Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Quackenbush, J. and Keele, J.W.
Quackenbush, J. and Keele, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
                                                                                                                                                                                                                                                                                                                      Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
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Plate: 52 row: G column: 21
Seq primer: ATTTAGGTGACACTATAG
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/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
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                                                             GTGTCTGCAAGCCCGCTGC
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                                                                                                                                                                                                                                                    Conservative
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/clone lib="MARC 1PIG"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
/ibrary made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                                                                                                                                                                                                                                  54.9%;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                855 California Ave, Palo
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                   Contact: Walbot V
Department of Biological Sciences
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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/mol_type="mRNA"
/strain="FVB/N"
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/lab_host="DH10B"
/mol type="genomic DNA"
/cultivar="mixed background
/db_xref="taxon:4577"
/tissue_type="leaf"
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/clone="IMAGE:3983528"
                                                                                                               organism="Zea mays"
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/mal_type="genomic DNA"
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/clone="BACN15K14"
     clone_lib="DrosBAC"
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AL106545.1 GI:5622456
GSS.
Submitted (33-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ bases 1 to 1201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genome survey sequence T7 end of B
BACN15K14 of DrosBAC library from Drosophila melanogaster
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/clone_lib="108 - RescueMu Grid I"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
pBlueScript backbone); Modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.rmdb.iastate.edu and follow the links for
'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
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/lab_host="DH10B"
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Pred. No. 55;
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FEATURES
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LOCUS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
                 Vascular Plants; project phase
Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
                                                                                     Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulat Vascular Plants; project phase 2
                                                                                                                                                                                                                  BG845919.1 GI:14227103
BG845919.1 GI:14227103
EST.
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonacacee; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                BG845919 T30 bp mRNA linear EST 29-MAY-2001
1024011F06.x1 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlanydomonas reinhardtii cDNA, mRNA sequence.
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University
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/dlone="GSDD1074YC24"
/clone="GSDD1074YC24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone="Tat strand cDNA was primed with a NotI-cligo(dT)
/note="Tat strand cDNA was primed with a NotI-cligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/mol_type="mRNA"
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16.3%;
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Pred. No. 5
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Fax: 919 613 8177
Email: chauser@dul
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BF101158.1 GI
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Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 1454)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Conso
DNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics of the Conso
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DNA Sequencing by: Incyte Genomics
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chauser@duke.edu
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/mol type="mRNA"
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/gerain="CC-1590 wild type mt+ 21gr"
/db xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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Pred. No. 53;
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Sciurognathi; Muridae;
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musculus cDNA clone
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OSJNEC13F02.f OSJNEc Oryza sativa (japonica cultivar-group)
Clone OSJNEC13F02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
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FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 13 row: F column: 02
Seq primer: gta aaa cga cgg cca gtg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between rice and Magnaporthe grisea Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. Large-scale identification of ESTs involved in the interaction
                                 BH887860
LB01712a.d_SP6.1 Leishmania major Priedlin BAC Library Leishmania major genomic clone LB01712a, genomic survey sequence.
BH887860
BH887860.1 GI:22133383
GSS.
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1 (bases 1 to 835)
Leishmania major
                  Leishmania major
                                                                                                                                                                                                                                                                                                                 ATGCCGCCGGGTGTTCGACCGGATCGCGCACCCGACCTGCCGGCCTGGAACGCGCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="OSJNEc"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
/hoI; 6 hrs after innoculation with Rice Blast (C9240-1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="Nipponbare"
/db_xref="taxon:39947"
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/mol_type="mRNA"
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dev_stage="3 week"
lab_host="DH10B"
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Pred. No. 34;
0; Mismatches
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Myler, P.J., Vogt.C., Munden, H., R
Fazellnia, G., Aggarwal, G., Nelson
Stuart, K. and Ragland, M.
Leishmania major Friedlin BAC End
Unpublished (2002)
Other GSSs: LB01712a.d_T7.1
Contact: Myler PJ
Contact: Myler PJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                               459
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83; Conserv
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 206 284-8846
Fax: 206 284-0313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seattle Biomedical Research Institute 4 Nickerson Street, Seatttle, WA 9810 Tel: 206 284-8846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1108)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                  BX382084 linear ESBX382084 Homo sapiens PLACENTA COT 25-NORMALIZED Homo clone CS0DI074YC24 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mylerpj@sbri.org
                   Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                         Contact: Genoscope
                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                              BX382084.1
Email: seqref@genoscope.cns.fr,
                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACTGGTCACTGTGGTCATCGTCTCCGTGGCCATCTCA 421
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/strain="Friedlin"
/db_xref="taxon:5664"
/clone="LB01712a"
/lab hosr-""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Clone lib="leishmania major Friedlin BAC Library"
/note="Vector: pCG270; Site 1: HindIII; Genomic DNA from
Leishmania major Friedlin in agarose blocks was partially
digested with HindIII, size selected, and ligated with
HindIII-digested pCG270 vector DNA. 10368 clones were
picked and arrayed in 384- and 96-will plates. Library
construction and arraying was carried out by ResGen
Corporation and clones and filters are available from
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Pred. No. 46;
0; Mismatches
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Nelson,S., Seyler,A.,
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  Web : www.genoscope.cns.fr
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Best Local
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ALOS3013
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AL053013.1 GI:4934461
GSS.
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                TTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACTGCGGCCAGGCCCGC
                                                                                                                                                                                                                              CSCCTCCCSYSYSSSTSSSSSTSWGSTSGSSSSSGTSTSGSSSDSTSTCCSCCYMCTCCST
                                                                                                                                            CCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAAACCCCATTGCCCG
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                                                                                                                                                                                                                                                                                                                                                                    Conservative 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/mol_type="genomic ZOA"
/db xref="taxon:7227"
/clone="BACR19D16"
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"end : TET3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com t
http://fullength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO79DG08NP1.
Location/Qualifiers
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BX361080 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI079YN16 3-PRIME, mRNA sequence.
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BP 191 91006 EVRY cedex - France
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1 (bases 1 to 1201)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                        KKKKKKKCCCCBKBCCCCKYKCCKBKKYCCYKCKKKKKCKKKYCCCBCCCKKKCBCYCC 1124
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/mol_type="mRNA"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147;
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RESULT 5
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Matches 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2, cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR20K04 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bubaryota, Metazoa, Arthropoda; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Enydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                            GCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTTGTGGTAATTCC
                                                                                                                                                                                                                                                      CTACTTCGTCCTTTCSTCTTTMGTTGTAAMKWGKMWCTTGGAATCCKCTKYAGARARAAC
                                                                                                                         AGGTCAGGCCTATTTGCGGCGCGCTGCTGATCTTCTTGGGTCTGTTGA 718
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                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RPCI-98"
/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="BACR20K04"
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Pred. No. 14;
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                                                        1040 MANAMICKANVMKKKKWCKKKBMSKKMMMIKKVCKMBBMCMSKGGCMMCGCMCKGCVGCMI 1099
                                                                                                                                                                              980
                                                                                                                                                                                                                                419 CTGCGGCCAGGCCGCAGGCTGGTCGGCGACTTATCTCAATGCAAATAGCGTTTC
                                                                                                                                                                                                                                                                                                                                                         359 AAAACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCA 418
                                                                                                                                                                                                                                                                                                                                                                                                                  860 MMMIKNKAMMKKDNIMMMMMCAMMCIMMKKNIMMMBKKNICHMKKMCCIMMKKKKKHKKNIMMKK 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com |
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI072CC03NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX381961 1201 bp mRNA linear EST 08-MAY-200 BX381961 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI072YF05 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX381961.1 GI:30453007
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1 (bases 1 to 1201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MCCMCKKKKOMBKGKOVCMCKNAMKNKKCMCMKBMMACKMCMKMCMBKKONMAMAMKMKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGCIGCAGGITIGGGCATGTACCCGATTGGTATTGCGTTTTGGTCTCTTGGTTATTCAAT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAACCTCCC 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MANNICN CNKKKANNKT NIMINNAMINNIN KKANINNIN KANINNIN NININ INTERNAS KCKKKKAMCCK
                                                                                                                                                                              VKKVMCMCDBKMCMCKKKBMKKVCCKKMCMMMMMCAMKVMMMBAMMMBAMVVMMMMN 1039
AAATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCT 598
                                                                                                                                                                                                                                                                                                MMICKKBMICKKNKMINKMIVKKKKAMMIBKCVMKMKMKMCCKKKVMMBKMCAKKKKMCMC 979
                                                                                                              ACTCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTG 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 6.3%; Pred. No. 19;
Conservative 210; Mismatches
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR \
sites of the pCMVSPORT 6 vector. Library was normalized
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Eutheria; Primates;
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Pred. No. 19;
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Class:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BX356664 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COT 25-NORMALIZED Homo sapiens CDNA Clone CSODIO15YB03 3-PRIME, MRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com |
http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODI015CA02NP1.
Location/Qualifiers
                                                                                                                                                   1 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)
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                                                                     GTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGG
STBSTSSTTSTBTSCTTTBSSTTBYTBSSSYBSBSSBTTSSCSCTSSBSTTSSTBSMTSS
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                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="CSODIO15YB03"
/clone="CSODIO15YB03"
/clone=Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone=Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Tist strand cDNA was primed with a NotI-oligo(dT)
/note="Tist strand cDNA was primer. Five prime end enriched, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/mol_type="genomic DNA"

/db_xref="taxon:9606"
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/mol_type="mRNA"
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Pred. No. 0.00068;
0; Mismatches 77;
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AUTHORS
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JOURNAL
                                                              Query Match
Best Local Similarity
Matches 82; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 743)

whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics Unpublished (2002)

Other_GSSs: OGUAX55TV

Other_GSSs: OGUAX55TV
                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                   Seq primer: TR
Class: sheared ends
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                                                                                                                                                                                                                                                                                                                                 Email: whitelaw@tigr.org
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                                CCGCAGGCTGGTCGGCGACCTTATCTCAATGCAAATAGCGTTTCACTCCTACTGG
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                                                                                                                                        /clone="ZMMBMa0397J14"
/clone_lib="ZM 0.7_1.5KB"
/notee="Vector: pBCSK-, Site_1: HincII; 0.7-1.5
methylation filtered genomic_DNA library"
                                                                                                                                                                                                                       /mol_type="genomic
/strain="B73"
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                      db_xref="taxon:4577"
                                                                                                                                                                                                                                                    organism="Zea mays"
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                                                                             53.6%;
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pred. No. 13;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                         Score
54.6
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753
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Copyright (c) 1993 - 2004 Compugen Ltd.
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BX356664
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AQ936633 HSJ41-905
BX356664 BX356664
CC684922 OGUAX55TH
AL054013 Drosophil
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ALIGNMENTS

					COMMENT	PUBMED	MEDLINE	JOURNAL	TITLE				AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	AQ936633
 Fax: +46-8-337983	Tel: +46-8-728-6372	17177 Stockholm. Sweden	Karolinska Institute	Center for Genomics Research	Contact: Podowski RM	10710430	20175728	Nucleic Acids Res. 28 (7), 1635-1639 (2000)	NotI clones in the analysis of the human genome	Wahlestedt, C.	Li,J., Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and	Xie, L., Muravenko, O.V., Kozyrev, S., Petrenko, L., Skobeleva, N.,	Zabarovsky, E.R., Gizatullin, R., Podowski, R.M., Zabarovska, V.V.,	1 (bases 1 to 473)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)	GSS.	AQ936633.1 GI:7213011	AQ936633	sequence.	HSJ41-905 Human NotI clones Homo sapiens genomic, genomic survey	AQ936633 473 bp DNA linear GSS 23-AUG-2000	

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Search completed: April 17, 2004, 20:13:05 Job time : 88.0151 secs

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Sequence 1938, Application US/60548091

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES TH
FILE REFERENCE: CLO01506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTMARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1938
LENGTH: 201
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US-60-548-091-19934
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US-60-548-091-19938
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US-60-548-091-19938
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CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19934
LENGTH: 201
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
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Best Local Similarity 52.7
Conservative
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Local Similarity 52.7%;
hes 69; Conservative
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RESULT 14 US-10-767-701-9054

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CGTCGCTCAAGTACC 204

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; TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER IMPORMATION: Clone ID: 14593439
US-10-767-701-23189
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US-10-767-701-23189
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GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5355)B
FULE REFERENCE: 38-21(5355)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 9054
LENGTH: 1028
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CUTRENT APPLICATION NUMBER: US/10/767,701
CUTRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 23189
LENGTH: 519
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Local Similarity 52.6%;
les 71; Conservative
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Query Match Best Local Similarity 54.9

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322 GT 323

213 CT 212

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US-10-765-790-62

APPLICANT: APPLICANT:

Burgess, Chris Gannon, Allison Harvey, Jeanne Lechner, John F.

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APPLICANT: Li, Zheng
TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
EILE REFERENCE: 1657/2035
CURRENT APPLICATION NUMBER: US/10/765,790
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: US 10/737,082
PRIOR PILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 300
SOFTWARE: PatentIn version 3.2
SEQ ID NO 62
LENGTH: 23490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 62, Application US/10765790 GENERAL INFORMATION:
Sequence 5686, Application US/60548091
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, MICHELE AL.
APPLICANTION: STROKE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5686
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APPLICANT: Beard, Chris
APPLICANT: Burgess, Chris
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Pred. No. 0.53
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Pred. No. 3.8;
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CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/188,914
PRIOR TILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/192,033
PRIOR APPLICATION NUMBER: 60/192,033
PRIOR PILLING DATE: 2000-03-24
PRIOR PILLING DATE: 2000-04-14
PRIOR PILLING DATE: 2000-04-14
PRIOR PILLING DATE: 2000-04-24
PRIOR APPLICATION NUMBER: 60/207,702
PRIOR APPLICATION NUMBER: 60/207,702
PRIOR PILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-06-23
PRIOR PILLING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/21,849
PRIOR APPLICATION NUMBER: 60/21,849
PRIOR PILLING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 60/230,732
PRIOR APPLICATION NUMBER: 60/230,732
PRIOR PILLING DATE: 2001-09-07
PRIOR PILLING DATE: 2001-09-07
PRIOR PILLING DATE: 2001-09-07
PRIOR PILLING DATE: 2001-09-07
PRIOR PILLING DATE: 2001-02-07
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US-09-804-291A-500
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Best Local Similarity
Matches 68; Conserv
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SEQ ID NO 500
LENGTH: 930
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GENERAL INFORMAT
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Best Local Similarity 54.0%;
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TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
FILE REPERENCE: 100337.54287US
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33.2; DB 5;
Pred. No. 1.2;
0; Mismatches 58;
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, TYPE: DNA
; ORGANISM: Homo sapiens
US-10-765-790-62

Query Match Best Local :

y Match 4.5%; Local Similarity 49.7%; hes 86; Conservative

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21270

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RESULT 10 US-60-548-091-5686

TILE OF INVENTION: Huma

Human Secreted Proteins

e 983, Application US/10100683 INFORMATION:

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; ORGANISM: Homo sapiens
US-10-100-683-983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-100-683-11511
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Best Local S
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CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/043,576
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,845
PRIOR RICHARD AND 1007-05-23
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 13468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1997-04-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PS900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: Rosen, et al
                                                                        OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: US 60/043,580
OR FILING DATE: 1997-04-11
OR APPLICATION NUMBER: US 60/047,599
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: US 60/056,664
OR FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: US 60/043,580
FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/043,314 FILING DATE: 1997-04-11
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                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/043,576 FILING DATE: 1997-04-11
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PILING DATE: 1997-08-22
APPLICATION NUMBER: US 60/043,314
FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/047,632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF INVENTION: Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2360 CAGCTCCCGGCCCAGTGGTGGGCTCAGGGCTCCTGGGCGCCATGGGTCTCACCACA 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/056,892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1997-05-23
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ilarity 75.4%;
Conservative
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Pred. No. 0.79;
0; Mismatches
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US-10-100-683-11511
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OTHER INFORMATION: Clone ID: US-10-767-701-744
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NUMBER OF SEQ ID NOS: 13468
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11511
LENGTH: 7071
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Best Local S
Matches 62
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CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 7545
LENGTH: 666
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Best Local Similarity
Matches 43; Conserv
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                           NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 744
LENGTH: 561
Type: ""
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                                                                                                                                            TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                     APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
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                                 ORGANISM: Sorghum bicolor FEATURE:
                                                                         TYPE: DNA
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Cao, Yongwei
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75.4%;
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                   SORBI-28MAY03-CLUS124346_1
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Pred. No. 0.42;
0; Mismatches 46;
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Pred. No. 1
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NUMBER OF SEQUENCES: 7310

SPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street CITY: Waltham STATE: Massachusetts

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NAME/KEY: misc feature;
LOCATION: (B) LOCATION 1...768;
SEQUENCE DESCRIPTION: SEQ ID NO: 1266;
US-10-417-884A-1266
                                                          RESULT 3
US-10-767-701-5263
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APPLICATION NUMBER: US/10/417,884A
APPLICATION NUMBER: US/09/107,532
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532
FILING DATE: 30-Uun-1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: JUly 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELECAM: (781)893-5007
TELECAM: (781)893-5007
TELECAM: (781)893-5277
INFORMATION POR SEQ ID NO: 1266:
SEQUENCE CHARACTERISTICS:
IFRUTH: 768 base pairs
Sequence 5263, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
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                                                                                                                                               272
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                                                                                                                                                                                                                                                                                                                                                                                                                              107 TAAAAACCTCCCTTGCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104;
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OPERATING SYSTEM: <Unknown>
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                        TCGCGCTCACCACATTGCTGGTGAACTTCCG 317
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ilarity 49.3%;
Conservative
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RESULT 5 US-10-100-683-983/c

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US-10-767-701-10866
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 5263
LENGTH: 619
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5355)B
FILE REFERENCE: 38-21(5355)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NO 10866
LENGTH: 1034
TYDE: NA
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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ORGANISM: Sorghum bicolor
FEATURE:
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AAGGCCATCAGCCTCTCCGACGGCGACTTCACCGTCACCGACGCCAACGGCGCCGTC 327
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pred. No. 0.45;
0; Mismatches 89;
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Minimum DB
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
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Listing first 45 summaries
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                           US-10-767-701-10854
US-10-767-701-5263
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US-10-100-683-1933
US-10-100-683-11531
US-10-767-701-745
US-10-767-701-744
US-10-767-701-924
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US-10-767-701-1931
US-10-767-701-14711
US-10-767-701-132
US-10-775-920-136
US-60-555-303-656
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US-10-775-920-131
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Sequence 10854, A
Sequence 1266, Ap
Sequence 5263, App
Sequence 913, App
Sequence 11511, A
Sequence 7545, Ap
Sequence 7545, Ap
Sequence 62, App
Sequence 62, App
Sequence 500, App
Sequence 19934, A
Sequence 19934, A
Sequence 9054, Ap
Sequence 23189, A
Sequence 14711, A
Sequence 14711, A
Sequence 13767, Ap
Sequence 136, App
Sequence 137, App
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78-	5-8	8-0	1	85-	1-3	7-8	7-8	7-2	7-2	-5	57-	3-4	9-6	3-457	0-6	3-4	6.5	į
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ALIGNMENTS

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RESULT 2
US-10-417-884A-1266
US-10-417-884A-1266
; Sequence 1266, Application US/10417884A
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm
; APPLICANT: Lynn A DOUCELIC ACID
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; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS47627_1
US-10-767-701-10854
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SEQUENCE 10854, Application US/10767701

SEQUENCE 10854, Application US/10767701

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 10854

LENGTH: 1014
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US-10-767-701-10854
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Best Local &
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105; Conservative
                                                                                                                                                                                                                                                            311 ACTTCCGCCACGTATTCTATGCGTTTTCATTCC 343
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Pred. No. 0.007;
0; Mismatches 108; Indels
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and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

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; NAME/KEY: misc feature

; LOCATION: (1). ... (751)

; OTHER INFORMATION: n = A,T,C or G

US-09-439-313-12
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US-09-352-616A-12/c
; Sequence 12, Application US/09352616A
; Patent No. 6395278
; Patent No. 6395278
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                                                                                                                                                                                                                                                                                             ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(751)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-12
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT PILICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASE(SEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/352,616A CURRENT FILING DATE: 1999-07-13 NUMBER OF SEQ ID NOS: 472 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 12 LENGTH: 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.8%; Score 36.4; DB 4; Length 751; Best Local Similarity 59.8%; Pred. No. 0.11; Matches 58; Conservative 0; Mismatches 39; Indels
                                                                                                                                                                                              Query Match 4.8%;
Best Local Similarity 59.8%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jiang, Yuqui
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILB REFERENCE: 210121.42708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapien
                                                                                               410
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350
                                               287 TCGCGCTCACCACATTGCTGGTGAACTTCCGCCACGT 323
                                                                                                                                              227 CGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCCTGGGCGCCA 286
                                                                                               CGTTCTTCATCNTCCTCNTCATCTTCATTGCTGAGGTNGCAGCTGCTGTGGTCGCCT 351
TGGTGTACACCACAATGGCTGAGCACTTCCCTGACGT 314
                                                                                                                                                                                              Score 36.4; DB 4; Length 751; Pred. No. 0.11; 0; Mismatches 39; Indels
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Search completed: April 19, 2004, 18:38:27 Job time : 68.4023 secs

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US-09-020-956-12/c
; Sequence 12, Application US/09020956
; Patent No. 6261562
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2761
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                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: cDNA
US-09-020-956-12
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PRIOR APPLICATION NUMBER: US:
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2761
LENGTH: 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atent No. 6261562
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
COPERATE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/020,956
APPLICATION NUMBER: US/09/020,956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: OUT STREET: SEATTLE CITY: Seattle TTATE: WA
                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                        STRANDEDNESS: si
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1333 GCCGCCCAGGCCACCTTCCTGGTCACCGCGCTGGTCTACTTCTGCTACG 1384
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    CGTTCTTCATCNTCCTCNTCATCTTCATTGCTGAGGTNGCAGCTGCTGTGGTCGCCT 351
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59.8%;
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                                                                           Score 36.4; DB 3;
Pred. No. 0.11;
0; Mismatches 39;
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                                                                               39;
                                                                               Indels
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TCGCGCTCACCACATTGCTGGTGAACTTCCGCCACGT 323

บร-09-439-313-12/c

Sequence 12, Ap. 8329

Application US/09439313

GENERAL INFORMAT APPLICANT: Xu,
APPLICANT: Di
APPLICANT: Mi
APPLICANT: Ha

Dillon, Davin C. Mitcham, Jennifer L.

Susan

Louise

APPLICANT:

Jiang Yuqui Reed, Steven G. Kalos, Michael Fanger, Gary Retter, Mark Solk, John

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US-09-030-607-12/c
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GENERAL INFORMATION
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                                                                                                                                                     Best Local Similarity Matches 58; Conserv
                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Jiangcnun C. APPLICANT: Dillon, Davin C. TITLE OF INVENTION: COMPOUN 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Re-Lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                              227 cgagerecaccaaaarecragrearearecrecregragacacaaacacceccaaacacca 286
350 TGGTGTACACCACAATGGCTGAGCACTTCCCTGACGT 314
                                                                          CGTTCTTCATCNTCCTCNTCATCTTCATTGCTGAGGTNGCAGCTGCTGTGGTCGCCT 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                        4.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   210121.427C3
                                                                                                                                                   Score 36.4; DB 3; Length 751; Pred. No. 0.11; 0; Mismatches 39; Indels
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RESULT 8
US-09-252-991A-11418
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Matches
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NUMBER OF SEQ ID NOS:
SEQ ID NO 11418
LENGTH: 1086
                                                  GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
APPLICANT: GENERIOS: ESTS and Encoded Human
FILE REFERENCE: GENERIO-054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Marc J.
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                                                                                                                                                                                                    Sequence 8976, Application US/09621976 Patent No. 6639063
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NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 8976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                     GTGCCGGGTTCTTTTCGATCATCTTCACCACCCTCCTCCTGACCTCGCAGCACCTGCTCT
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                                                                                                                                                                                                                                                                                                                 ACGGCATGAGCTTGCGGCCG 361
                                                                                                                                                                                                                                                                                                                                                  ATGCGTTTTCATTCCCGCTG 348
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nilarity 55.0%;
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                                                                                                             and Encoded Human Proteins.
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3205
LENGTH: 1100
TYPE: DNA
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US-09-621-976-8976
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US-09-252-991A-3205/c
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US-09-252-991A-2761
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                                                                                                             Sequence 2761, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: ACID SEQUENCES RELATING TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074.788
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILB REFERENCE: 107196.136
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RESULT 6
US-09-107-532A-1266
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US-08-232-463-14
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Sequence 1266, Application US/09107532A

Patent No. 6583275

Patent No. 6583275

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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                              COUNTER: CD/ROM ISO9660
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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     COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
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                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. RUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                            SEQ ID NO 11376
LENGTH: 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11376, Application US/09252991A Patent No. 6551795
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LENGTH: 768 base pairs
ORGANISM: Pseudomonas aeruginosa
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPAX: (781)893-8277
TELEPAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
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STRANDEDNESS: double
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Pred. No. 0.0092;
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Best Local S
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ORGANISM: Corynebacterium glut
FEATURE:
NAME/KEY: gene
LOCATION: (101)...(853)
OTHER INFORMATION: brnF
NAME/KEY: gene
LOCATION: (853)...(1176)
OTHER INFORMATION: brnE
OTHER INFORMATION: brnE
OTHER INFORMATION: ATCC13032
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Sequence 3016, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
APPLICANT: GATY BRETON ET. AL
ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PRIVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-2004001

FILE REFERENCE: 2709-2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 756

TUDE: CNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Klebsiella
US-09-489-039A-3016
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RESULT 5
US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 7.8%;
Local Similarity 52.2%;
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                                                                        CTTCACTGC 310
                                                                                                      TTTCATTCC 343
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Pred. No. 8.6e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 756;
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RESULT 5
US-08-232-463-14
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
Patent No. 5670367
Patent No. 5670367
APPLICANT: DORNER, F.
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: BORNER, F.
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION UNMBER: US/08/232,463
FILING DATE:
APPLICATION NUMBER: US/07/935,313
APPLICATION NUMBER: EP 91 114 300.6
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RESULT 4 US-09-489-039A-3016

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Sequence 1, Application US/09471803A

| Sequence 1, Application |
| Patent No. 6613545
| Patent No. 6613545
| Patent No. 6613545
| Patent No. 6613545
| Patent No. 6613545
| Patent No. 6613545
| Patent No. 6613545
| Patent No. 1071AR
| APPLICANT: SAHM, HERMANN
| APPLICANT: SAHM, HERMANN
| APPLICANT: SCAHM, LOTHAR
| APPLICANT: BEGELING, LOTHAR
| APPLICANT: BEFFRENCE, WALTER
| TITLE OF INVENTION: NUCLECTIDE SEQUENCE CODING FOR THE EXPORT OF
| TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
| TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
| FILE REFERENCE: 21133/265496/WAS
| CURRENT PILING DATE: 11999-12-23
| PRIOR APPLICATION NUMBER: US/09/471,803A
| CURRENT PILING DATE: 1999-12-23
| PRIOR APPLICATION NUMBER: DE 199 51 708.8
| PRIOR FILING DATE: 1999-10-27
| NUMBER OF SEQ ID NOS: 12
| SOCTWARE: PatentIn Ver. 2.1
| SEQ ID NO 1
| LENGTH: 1271
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                                                                                                    NAME/KEY: gene
LOCATION: (853)..(1176)
OTHER INFORMATION: brnE
OTHER INFORMATION: ATCC14752
US-09-471-803A-1
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Query Match
Best Local Similarity 100.0%;
Matches 753; Conservative
                                                                                                                                                                                                                              NAME/KEY: gene
LOCATION: (101)...(853)
OTHER INFORMATION: brnf
                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Corynebacterium
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
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        Score 753; DB 4; 1
Pred. No. 2.9e-231;
; Mismatches 0;
                                                        Length 1271;
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  Sequence 6, Application US/09471803A

Patent No. 6613545

GENERAL INFORMATION:
APPLICANT: KENNERKNECHT, NICOLE
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
APPLICANT: PREFERELE, WALTER
TITLE OF INVENTION: NUCLECTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/265496/MAS
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
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PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR PRIOR PRIOR DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTING DATE: 1999-10-27
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APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: HERACHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/265496/MAS
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 753
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Patent No. 6613545
GENERAL INFORMATION:
APPLICANT: KENNERKNECHT, NICOLE
APPLICANT: SAHY, HERMANN
APPLICANT: BEGELING, LOTHAR
APPLICANT: PFEFFERLE, WALTER
                                                                                                                                                                                                                                                                     ; LOCATION: (1)..(753)
; OTHER INFORMATION: brnF
; OTHER INFORMATION: ATCC14752
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TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(753)
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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RESULT 15
AAA10594/c
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DT 29-JUN-2000 (first entry)

XX
DE Gene encoding a subunit of cellulos

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DE Gene encoding a subunit of cellulos

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DE Gene encoding a subunit of cellulos

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DE Gene encoding a subunit of cellulos

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DE Cellulose synthase; cellulose produ

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DE Vigna angularis.

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Best Local S
Matches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that one was to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10732 BP; 3149 A; 1212 C; 2074 G; 2046 T; 0 U; 2251 Other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cellulose synthase; cellulose production; increase yield; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 14-21; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene encoding a cellulose synthetic equipment - for the improvement he amount of cellulose synthesized in a plant body.
9649 TISRCTBYSTBTBTTSRCAKCTBDSTSTAKNSTSTYSTTRCTBYSSRSRGYSYCSRSRSR 9590
                                                                                                                                        9709
                                                                                                                                                                                                                                                                         9769 GYDANSTSRYSSRYSSTYSSDSTYSAKYCAKSTTBTBCYYDAYDACYDAYDANCYSSDST 9710
                                                                                                                                                                                                                                                                                                                                                                                                                         9829 SDSTSTYRCSRSDYDATBSDNSTNCCYDASRTBTBSTNCYARCYTBYDARCSRDSTYSSR 9770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9949 RYSSTCHCYSYCCYTSRYSSTTINSTCRCTTYSYNSTTBTBYSYSSTYSSRGYSSRGSDS
                                                            502 CTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAAATTAAGGGCCTCG-AGTTCGC 560
                                                                                                                                                                                                                                                                                                                                                 442 TCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCACTCCTACTGGGTATTCGGCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 GTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAAACCCCATTGCCCGTTTCTAT 381
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Similarity 14.7%; Pred. No. 0.13;
54; Conservative 182; Mismatches 189; Indels 1;
                                                                                                                                    YTBYCSRRCCCYYDAYSCSRYDARCYDACYSYSNSTCYDATBTTSRYSTTYSYYSNCYDA
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Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acids, by fermenting the amino acid-producing coryneform in whice at least the lrp gene has been weakened or amplified, then isolating amino acids that have accumulated in the medium or cells. (I) is used transform coryneforms for production of L-amino acids, specifically lysine and isoleucine, which are used in medicine and particularly as animal feed supplement. It may also be used as probes and primers for isolating related sequences. Regulating expression of (I) improves production of amino acids, especially of L-lysine. This sequence encod the Corynebacterium glutamicum lrp protein which is used in the method described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel isolated nucleic acid (I) from coryneform bacteria used for the fermentative production of selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New 1rp gene from coryneform bacteria, used to prepare transformants with increased synthesis of amino acids, particularly lysine and isoleucine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 715
                                   Chang H, C
Katagiri F,
                                                                                                                                                                                                              Plant; bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                    Rice gene,
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                                                                                                                                                                                                                                                                                 ADA71938;
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               WPI; 2003-175290/17
                                                                                                             22-JUN-2001;
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                                                                                        22-JUN-2001; 2001WO-IB001105
                                                                   (SYGN ) SYNGENTA PARTICIPATIONS
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                                  Chen W, Co
F, Quan S,
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S, Tao Y,
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Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                       gene expression.
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Claim 27; OES 占 NO 5263; 899pp; English

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

Query Match Best Local S Matches 75

75; Similarity

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Score 47; DB 7 Pred. No. 0.001 28; Mismatches

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Length 2000; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCATCGCCCT-----CGTTGTGGGCGCAGCGCCCCTGGGGCGCCATCGCGCTCACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCYCWRYATCYWCCCYRKRGWYSRRSMMRTAGKWKMRSWSRWCRSYSWYKMYKKMWKKSY
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                                                                                                                                              CCKKYCSCCTKYCSYTGYYRYCKWYKYSYYKCYYCYCYWYMSYMRYMMKCMCSRSCSSWM
                                                                                                                                                                                                                   GCCGAACGAAAAAGCAGATCCCTTCTCTGCTGCTGCAGGTTTGAGCTTCACCATTGCTC
                                                                                                                                                                                                                                                                                            SKWKYMSKSCSMRMTCSSWCSCCYTCYYGAMCWSCCMSMMYMGSCGCYTRGWKWRSKYSM
                                                                                                                                                                                                                                                                                                                                                     AAATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCT
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   SCAYCSTSSTSRWMSMYYAAKWGMCGSSGMYRMSKSCKMYSKYSSCKYTGSKKCTKRKYY
                                                                        TTGTGGTAATTCCAGGTCAGGCCCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                  YMSYGWARSSGTWSRSAAKRTYKGYSTSRRAKMMRACRMYSACRRYSRTSYYCGCSYCGS
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RESULT 12
ACA01968
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Matches 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 309400 BP; 70133 A; 86477 C; 83115 G; 69675 T; 0 U; 0 Other.
                                                                                                         04-JUN-2003
                                                                                                                                 ACA01968;
                                                                                                                                                            ACA01968 standard;
                           Corynebacterium
                                                    Coryneform;
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                                                                               glutamicum
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                                                                                                                                                                                                                                                                                                                                                                                                         AAATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTTGTCACGCTGACTTTGGATTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCCCATTGCCCGTTTCTATTCGCTTTTTCGCGCTTATCGAAGCCTACGCAGTCACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAAA 241
                                                                                                                                                                                                                              TTCTCCGCGTCCGCTTC 289353
                                                                                                                                                                                                                                                                                                           TTGTGGTAATTCCAGGTCAGGCCCTATTTGCGGCCGCTGCTGATCTTCTTGGGTCTGTTGA
                                                                                                                                                                                                                                                                                                                                       TCAAAAATAACAAGGATTATTCGCTGCCATTATTCGCGGTGGTATTGGCTCTGGTTTTCCG
                                                                                                                                                                                                                                                                                                                                                               GCCGAACGAAAAAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTC
                                                                                                                                                                                                                                                                                                                                                                                         ATCTAAAAGGCATGGATTTTGCCCCTGACCGCGCTGTTTGTGGTGCTGGCGTGGGAGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCCAGGCCCGCAGGCTGGTCGGCGTG---GCGACTTATCTCAATGCAAATAGCGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCATGGTGAATTTCCGCCACATTTTCTACGGTCTCACCTTCCCACGCCACCGCCTCAAGT 289730
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                                                                                                                                                                                                                                                      CCATCCGGTACTTCTTC 735
                                                                                                                                                                                                                                                                                 GTTTTGTGGCGCCCGAGCAGATGCTGGTTATCGCTTTGACCACGTACTTTTTGATCCTTC
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                                                      nucleic acid array;
                                                                                                         (first entry)
                                                                               derived ORF SEQ ID 1959.
                            glutamicum
                                                                                                                                                              DNA;
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                                                                                                                                                              177
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                                                                                                                                                              ₽₽
                                                       fermentation;
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les 296;
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                                                       culture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 309400;
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Matches 106
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                                                                                                                                                                                                                                                                       .
                                                                                                                                                                                                                                 medicine;
                                                                                                                                                                                                                                                                                                                            AAF61688;
                                                                                                                                                                                                                                                                                                                                                     AAF61688
                             11-APR-2001.
                                                       EP1090993-A1
                                                                                                                                 -10_signal
                                                                                                                                                                                                                                                                                                                                                                                                                       132
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29-SEP-2000;

2000EP-00121159

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This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid array useful for Corynebacterium glutamicum during from Corynebacterium glutamicum.
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                                                                                                             Key
-35_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 177 BP; 54 A; 40 C; 47 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 647; 709pp; German.
                                                                                                                                                                             Corynebacterium glutamicum
                                                                                                                                                                                                                                       Fermentation;
                                                                                                                                                                                                                                                                                                                      12-JUL-2001
                                                                                                                                                                                                                                                                             glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106;
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                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTC
                                                                                                                                                                                                                      ion; L-amino animal feed
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            /*tag= a
88..93
/*tag= b
151..615
/*tag= c
                                                                                                                 Location/Qualifiers 62. .67
product=
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100.0%; Pred. No. 1.5e-22;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                       acid
                                                                                                                                                                                                                    supplement;
                                                                                                                                                                                                                                                                                                                                                                                                       715
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"בקס"
                                                                                                                                                                                                                                                                               DNA.
                                                                                                                                                                                                                                         production;
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                                                                                                                                                                                                                        ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bathe
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                                                                                                                                                                                                                                         gene;
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                                                                                                                                                                                                                                           lysine;
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Best Local S
Matches 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 711 BP; 123 A; 190 C; 198 G; 200 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 456; 709pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid array useful for Corynebacterium glutamicum during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Farwick M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUN-2001; 2001DE-01028510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glutamicum derived ORF SEQ ID 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003-279970/28.
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                                TCATGGTGAATTTCCGCCACATTTTCTACGGTCTCACCTTCCCACGCCACCGCATCAAGT
                                                                                                                          TTCTGGCAATCGGCATGGTCACCGCAGGTATCGGCCGCTTTTCGGCGGCGGTCGCTGGTT
                                                                                                                                                                        TGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCCTGGGCGCCATCGCGCTCACCACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid array; fermentation; culture;
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 6.3e-29;
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. are useful for identifying the mutation point of a gene derived from mutant of coryneform bacterium, measuring expression amount and anal the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived
                                                                                                                                                                                                           Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                       Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-DEC-1999; 99JP-00377484.
07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coryneform bacterium; amino acid
                                                                                                                                                                   Disclosure; SEQ ID NO 7069; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium
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                                                                                                                                                                                                                                                                                                             WPI; 2001-376931/40.
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Best Local Similarity 98.6
Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel isolated nucleic acid (I) from coryneform bacteria used for the fermentative production of selected L-amino acids, by fermenting the amino acid-producing coryneform in which at least the lry gene has been weakened or amplified, then isolating amino acids that have accumulated in the medium or cells. (I) is used to transform coryneforms for production of L-amino acids, specifically lysine and isoleucine, which are used in medicine and particularly as animal feed supplement. It may also be used as probes and primers for isolating related sequences. Regulating expression of (I) improves production of amino acids, especially of L-lysine. This sequence encodes a fragment of the Corynebacterium glutamicum lrp protein which is used in the method described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 778 BP; 175 A; 208 C; 207 G; 188 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                              Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH68373 standard;
                                                                                                                                                                                                                                 Corynebacterium
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Pred. No. 2.3e-74;
0; Mismatches 4;
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Nakagawa Tateishi 03-AUG-2000; 2000JP-00280988 (KYOW) KYOWA HAKKO KOGYO z 'n Mizoguchi Senoh A, i H, Ando Ikeda M, Ķ S, Hayashi Ozaki A; Σ Ochiai ~ Ξ

Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene gene.

8 SEQ ID NO 3408; 246pp + Sequence Listing; English.

The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly 1-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office

Sequence 711 BP; 123 A; 190 C; 198 G; 200 T; 0 U; 0 Other;

16.9%;

Length

711;

문 S 먉 S 맑 8 밁 Ś 片 Ś 밁 Ś 밁 S 밁 8 밁 5 Matches Query Match Best Local Similarity Matches 318; Conserv 173 182 122 413 353 422 293 362 233 302 242 533 473 539 479 53 GCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGGCTCCACCGAAA 241 CGGTCGGTTTGGGGGCTGATTCCGCTGGGTTTGGCCTTTTGGGCTGTTGATGGTCCAGACAG CTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATACG CGGCCAGGCCCGCAGGCTGGCGTG---GCGACTTATCTCAATGCAAATAGCGTTTC ccegcecceccianicacciacecinacecentecciacecinacecentecers ACCCCATTGCCCGTTTCTATTCGGTTTTCGGCGTTATCGACGAAGCCTACGCAGTCACTG rrcreecaarcecareercaccecaestatcesccccrrrrcesccecceccerrerr TGCTGGTCATCGCCCTCGTTGTGGGCGCCAGCGCCCTGGGCGCCATCGCGCTCACCACAT ĊAĠĊĊĊĠĊĊAĊĊŢĠĠĊĠAŢAŢĊAĠŢĠĊAĊĠĊĠĠĠŢĠĊŢŢAĊĊĠŢŢĊĀĀĀŢŢŢŢĠŢĠĊĊ TCATGGTGAATTTCCGCCACATTTTCTACGGTCTCACCTTCCCACGCCACCGCATCAAGT TGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAA TCAAAAATAACAAGGATTATTCGCTGCCATTATTCGCGGTGGTATTGGCTCTGGTTTCCG AAATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTCTTTGTCACGCTGACTTTGGATTCCT ACTCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTG GCCGAACGAAAAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTC Conservative Score 127.4; DB 5; Pred. No. 6.3e-29; 0; Mismatches 296; Indels w --Gaps 538 658 532 598 472 412 478 352 421 292 361 232 301 112 592

16-DEC-1999; 99JP-00377484 07-APR-2000; 2000JP-00159162

99JP-00377484

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TIGIGGTAATICCAGGTCAGGCCCTATITIGCGGCGCTGCTGATCTTCTTGGGTTGTTGA

18-DEC-2000; 2000EP-00127688

20-JUN-2001

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ID AAF61693;
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                                                                                                                                                                                                                                                        Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                    Fermentation; L-amino medicine; animal feed
                                                                                                                                                                                                                                                                                                                                                                     C. glutamicum
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                                                                         05-OCT-1999;
                                                                                                                    29-SEP-2000; 2000EP-00121159
                             (DEGS ) DEGUSSA-HUELS
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                                                                                                                                                                                                                                                                                                    acid production; lrp gene; lysine;
supplement; ds.
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Pred. No. 2.7e-161;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 G; 162 T; 0 U; 0 Other;
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Matches 276
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 397 BP; 96 A; 100 C; 104 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 16; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New lrp gene from coryneform increased synthesis of amino
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les 276;
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                                                                                                                                                                                                        GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT
                                                                                                                                                                                                                                                     GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG
                                                                                                                                                                                  GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAACCTCCCTT
                                                                                                                                                                                                                                                                                         GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG
   ATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCCTGG
                                                                         GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGGCCTGATTTTCGCGGGGCTCCACCGAA
                                                                                                              GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTTTGGTTATTCAATAC
                                                                                                                                   GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC
                                         GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAA
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Pred. No. 1.7e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bacteria, used to prepare transformants with acids, particularly lysine and isoleucine.
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                                                                                                                                                                                                                                                                                                                                               1.7e-74;
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YX EP1090
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XX OS-SEP
XX OS-OCT
XX ODEGS
                                                                                                                       Fermentation; L-amino medicine; animal feed
                                                                                                                                                                          12-JUL-2001
                                                                                                                                                                                              AAF61695;
                                                                                                                                                                                                                  AAF61695
                                                             11-APR-2001.
                                                                                EP1090993-A1
                                                                                                   Corynebacterium
                                        29-SEP-2000;
 (DEGS ) DEGUSSA-HUELS
                                                                                                                                                     glutamicum
                                                                                                                                                                                                                  standard; DNA;
                                         2000EP-00121159
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                                                                                                                                                    lrp encoding DNA fragment SEQ
                    99DE-01047792
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Matches 753;
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteriam are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, organic acids organic acids of the present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-376931/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 349980 BP; 79703 A; 91547 C; 98381 G; 80349 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; SEQ ID NO 1; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of nucleotide and protein
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acid synthesi
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                GCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCCGCGGCCTCCACCGAA
                                                                                                                                                                                                     GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC
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                TTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA
                                                                                                                       GGCTACGAATGGTGGGCAGCCCCACTGT
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TTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA
                                                           ATGCTGGTCATCGCCCTCGTTGTGGGCGCGCAGCGCCCTGGGGCGCCATCGCGCTCACCACA
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ilarity 100.0%;
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2000UP-00280988.
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Pred. No. 3.1e-222;
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                         This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polymucleotides. The arrays are used to corynebacterium glutamicum polymucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA0010-ACA0188 represent C. culture and fermentation conditions. ACA0010-ACA0188 represent C.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Coryneform;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium
                                                                                                                                       Claim 1; Page 647; 709pp; German.
                                                                                                                                                                               New nucleic acid array useful for Corynebacterium glutamicum during
                                                                                                                                                                                                                                                                               (DEGS ) DEGUSSA AG
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This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that concludes a polypeptide at least one of 251 amino acid (aa) (3) or 108 aa (5) colypeptides; (ii) encodes a polypeptide at least 70% identical with (3) cor (5); (iii) is the complement of (i) or (ii), or (iv) contains at least 15 consecutive bases from (i)-(iii). The invention also describes (a) protein derived from sequences of 753 bp (2) or 324 bp (4); (b) coryneform microorganisms, especially Corynebacterium, transformed with cone or more (I), where these are replicative DNA; (c) production of branched-chain L-aa by fermentation of coryneform bacteria in which the complete and/or brnf genes (or equivalent sequences) are amplified, composited that the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the seq
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                                                                                                                                                                                                                                                                                                                                                                                             New export genes from coryneform bacteria, useful for increasing fermentative production of branched-chain amino acids.
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                  Kennerknecht N,
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FORSCHUNGSZENTRUM JUELICH GMBH.
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P-PSDB; AAB86247, AAB86248.
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     ATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCTGC
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New export genes from coryneform bacteria, useful for increasing fermentative production of branched-chain amino acids.

This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that (c) is 70% identical with a sequence that (c) is 70% identical with a sequence that (c) polypeptides at least one of 251 amino acid (aa) (3) or 108 aa (5) crosscribes; (ii) encodes a polypeptide at least 70% identical with (3) crosscribes; (ii) is the complement of (i) or (ii), or (iv) contains at least 70% force of the form sequences of 753 bp (2) or 324 bp (4); (b) crosscribes (a) croyneform microorganisms, especially Corynebacterium, transformed with cone or more (I), where these are replicative DNA; (c) production of coryneform bacteria in which the branched-chain in-aa by fermentation of coryneform bacteria in which the branched-chain and/or branched-chain antino acids, crosscribes (a) specially overexpressed; and (d) method for isolating the brnE and/or specially enventative production of branched-chain antino acids, crosses yield of branched-chain and valine, which are useful in medicine and animal nutrition. (I) can also be used as source of primers and croynebacterium glutamicum ATCC 14752 brnF and brnE proteins described in the method of the invention

G; 360 T; 0 U; 0 Other;

Length 1271;

101 GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG 61 GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAACCTCCCTT 1 GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCCATCCAAGGCAGCCCTG GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT GCTGCAGGTTTGGGCATGTACCCGATTGGGTATTGCGTTTGGGTCTCTTGGTTATTCAATAC ATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCTGGGCGCCATCGCGCTCACCACA GCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAA GCGGCCAGGCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC GCGGCCAGGCCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTTCAC AACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT AACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT TTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA ATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCTGGGCGCCATCGCGCTCACCACA GGCTACGAATGGTGGGCAGCCCACTGTTTTCCGGCCTGATTTTCGCGGGGCTCCACCGAA TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA riegecareracecearregrarrecerrregrerecerriegrarreaarac Indels 0 Gaps 160 300 340 240 180 220 120 540 580 480 520 420 460 360 400 280 60 0

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07-APR-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakagawa
Tateishi
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Senoh A, Ikeda M,
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(c) 1993 - 2004 Compugen Ltd
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       This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) polypeptides; (ii) encodes a polypeptide at least 70% identical with (3) or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least 15 consecutive bases from (i)-(iii). The invention also describes (a) protein derived from sequences of 753 bp (2) or 324 bp (4); (b) coryneform microorganisms, especially Corynebacterium, transformed with one or more (I), where these are replicative DNA; (c) production of
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Claim 5; Page 14-15; 23pp; German.

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C. glutamicum brnF DNA.
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New export genes from fermentative production
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                                                                   WPI; 2001-391595/42.
P-PSDB; AAB86247.
                                                                                                                                Kennerknecht N, Eggeling L,
                                                                                                                                                                                                                                            27-OCT-1999;
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                                                                                                                                                                          (DEGS ) DEGUSSA AG. (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
  production
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  coryneform bacteria, useful for increasing on of branched-chain amino acids.
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Search completed: April 19, 2004, 18:30:10 Job time : 3194.51 secs
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Corynebacterium glutamicum
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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Sequence 7 from Patent EP1090993.
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AX137083.1 GI:14273428
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/mol type="unassigned DNA"

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/gene="Cgl0010"
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AATKIDSDIVAKGSRRLLFELDSLDGLWQEYQNGGTAADFGAHLEANSSTALDAILS
VADKNAESINVPGLGKYYKGYBGKAAKVIEQELPAIGQLIEKNAQ"
complement (10104. .11177)
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/protein_id="BAB97403.1"
/db_xref="GI:21322774"
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/transl_table=
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Sequence 1 from Patent EP1108790.
AX120085 AX114121
AX120085.1 GI:14036800
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Patent: EP 1108790-A 1 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
LOCATION,Qualifiers
1. .349980
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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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                                                                                                                                                                    TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA
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Pred. No. 1.2e-184;
Mismatches 0;
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SgS
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PF02768:DNA polymerase III beta subunit, C-terminal doma
TIGR00663:dnan: DNA polymerase III, beta subunit"
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subunit
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Best Local S
Matches 753
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/gene="brnE"
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/transl_table=
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/db_xref="GI:21311381"
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Co. I
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-MAY-2002) Satoshi Nakagawa, Kyowa Hakko I
Ltd., Tokyo Research Labbratories; 3-6-6, Asahi-machi,
Tokyo 19-8533, Japan (E-mail:snakagawa@xanagen.com,
Tel:81-44-829-3031, Fax:81-44-813-1651)
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Corynebacterium glutamicum ATCC 13032
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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AP005274.1 GI:21322764
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Corynebacterium glutamicum ATCC 13032 DNA,
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Direct Submission
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/codon_start=1
/transl_table=11
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/protein_id="BAB97394.1"
                                                                                                /gene="Cg10001"
/note="PF00308:Bacterial dnaA protein
TIGR00362:DnaA: chromosomal replication
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/strain="ATCC 13032"
/db_xref="taxon:196627"
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                                                                                                                                                                                                                                                                                        organism="Corynebacterium
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Query Match Best Local Similarity 100.0%; Score 753; DB 6; Length 1271; Best Local Similarity 100.0%; Pred. No. 1e-184; Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps Oy 1 GTGCAAAAAAGGCAAGAGATTCATTCAAGGCTGGAGGTGTCGCCATCCAAGGCAGCCCTG Db 101 GTGCAAAAAAAGGCAAGAGATTCATTCAAGCCTGGAAGGTGTCGCCATCCAAGGCAGCCCTG Oy 61 GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT Db 161 GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAAGGTCTAAAAACCTCCCTT Db 161 GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAAGGTCTAAAAACCTCCCTT Db 161 GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAAGGTCTAAAAAACCTCCCTT Db 161 GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAAGGTCTAAAAAACCTCCCTT Db 161 GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAAGGTCTCAAAAAACCTCCCTT Db 161 GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAAGGTCTCAAAAAACCTCCCTT Db 161 GAACCAGATGATAAAGGTTATCGGCGCTACGAAATTGGGTCTCTTGGGTTATTCAATACCTCCTTT	PREFERENCE PC (C12N15/09,C07K14/34,C12N1/21,C12P13/06,C PC (C12N15/09,C12R1:15),(C12N1/21,C12R1:15) PC (C12N15/00,C12R1:15) PC	method of isolating the same and utilization thereof patent; JP 2001169788-A 4 26-7UN-2001; DEGUSSA HUELS AG, FORSCHUNGSZENTRUM JUELICH GMBH OS COTYMEDIACTORIUM SILUTAMICUM ATCC13032 PN JP 2001169788-A/4 PD 26-JUN-2001 PD 26-JUN-2001 PF 24-CCT-2000 JP 2000324315 PR 27-CCT-1999 DE 19951708.8 PI NICOLE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, WALTER PI	method of isolating the same and utilization ACCESSION BD014994.1 GI:22555801 KEYWORDS JP 2001169788-A/4. SOURCE unidentified unclassified unclassified unclassified. REFERENCE 1 (bases 1 to 1271) REFERENCE 1 (bases 1 to 1271) Nucleotide sequence encoding the discharge of	Qy 721 ATCCGGTACTTCTTCGTGGAAAAGGCTGCTAAA 753	OY 601 CGAACGAAAAGCAGATCCCTTCTCTGCTGCTGCAGGTTTGAGCTTCACCATTGCTCTT	Db 581 TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCAGAGTTGATTCCTTTTGAA OY 541 ATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCTGC Db 641 ATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCTGC
0; MED MED MED MED MED MED MED MED MED MED	12P13/06,C12P13/08// ,(C12P13/06,C12R1:15), RESULT 12 AP45403/c LOCUS LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	BH Db OV ON ON ON ON ON ON ON ON ON	thereof. Db Oy Pfefferle,W. Cy branched amino acid, Db	Qy Db Orange PAT 27-AUG-2002 Db Dranched amino acid, Qy	TGAGCTTCACCATTGCTCTT 660	AGTTGATTCCTTTTGAA 640 AGTTGATTCCTTTTGAA 640 TGACTTTGGATTCCTGC 600 AGTTGGTTTGGATTCCTGC 700 Db
Lwo-gene-encoded member of a new Laiston J. Bacteriol. 184 (14), 3947-3956 (2002) 22077265 12081967 2 (bases 1 to 2105) Kennerknecht,N., Eggeling,L. and Sahm,H. Direct Submission Submitted (07-NOV-2001) IBT-1, Forschungsz Juelich 52425, Germany Location/Qualifiers 1. 2105 /organism="Corynebacterium glutan/mol_type="genomic DNA"	AF454053 Corynebacterium glutami regulator (lrp) genes, AF454053.1 GI:21311379 Corynebacterium glutami Corynebacterium glutami Bacteria; Actinobacteri Corynebacteria; Hotinobacteri Corynebacterinea; Corynebacteria; Actinobacteri 1 to 2105) Kennerknecht, N., Sahm, I Eggeling, L Export of L-isolauche	661 GTGGTAATTCCAGGTCAGGCCCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACC 720	581 TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGAATCGCAAGTTGATTCCTTTTJAA 640 541 ATTAAGGGCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCTGC 600 [361 ARCCCATTGCCGTTTCTATTCGGTTTTCGGGTTTTCGACGAGGCTACGCAGGCTACGCAGGCTACGCAGGCTACGCAGGCTACGCAGGCTACGCAGGCTACGCAGGCTACGCAGGCTACGCAGGTCACT 520 461 ARCCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCCAATGCAAATAGCGTTTCAC 480 421 GCGGCCAGGCCGCAGGCTGGTCGGCGTTGGCGAATTCCAATGCAAATAGCGTTTCAC 480	1 ATGCTGGTCATCGCCCTCGTTGTGGGCCCAGGCCCCTGGGGGCCCATCGCCCTCACCACA	

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RESULT 10
BD014991
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DEFINITION
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BD014991 1271 bp DNA linear PAT 27-AUG-2002 Nucleotide sequence encoding the discharge of branched amino acid,
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RS Kennerukunehito,N., Sahm,H., Eggering,L. and Pfefferle,W.

Nucleotide sequence encoding the discharge of branched amino acid,

method of isolating the same and utilization thereof

AL Patent: JP 2001169788-A 1 26-JUN-2001;

DEGUSSA HUELS AG,FORSCHUNGSZENTRUM JUELICH GMEH

OS COrynebacterium glutamicum ATCC14752

PN JP 2001169788-A) 1

PP 24-OCT-2000 JP 2000324315

PF 24-OCT-1999 DE 19951708.8

PR 27-OCT-1999 DE 19951708.8

PR 27-OCT-1999 DE 19951708.9

PC C12N15/09,C12R1:15),(C12N1/21,C12P13/06,C12P13/06,C12P13/06,C12N15/00,C12R1:15),(C12N1/21,C12P13/06,C12P13/06,C12P13/06,C12P13/06,C12N15/00,C12R1:15)

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/mol_type="unassigned_wa" /db_xref="taxon:1718" /note="ATCC13032" 101856 /note="unnamed protein product; brnF" /codon_start=1 /trans[_table=11 /trans[_table=11 /protein_id="cAC19927.1" /db_xref="GI:14273894" /db_xref="GI:14273894" /db_xref="REWTREMBL:CAC19927" /db_xref="REWTREMBL:CAC19927" /db_xref="REWTREMBL:CAC19927" /db_xref="REWTREMBL:CAC19927" /db_xref="REWTREMBL:CAC19927" /db_xref="REWTREMBL:CAC19927" /db_xref="REWTREMBL:CAC19927" /db_xref="REWTREMBL:CAC19927" /db_xref="REWTREMBL:CAC19927" /db_xref="REWTREMBL:CAC19927" /db_xref="REWTREMBL:CAC19927" /db_xref="REWTREMBL:CAC19927" /db_xref="REWTREMBL:CAC19927" /db_xref="REWTREMBL:CAC19927" /db_xref="REWTREMBL:CAC19927" /db_xref="GI:14273894" /db_	SOURCE Corynebacterium glutamicum ORGANISM Corynebacterium glutamicum Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae; Corynebacteridae, Actinomycetales, REFERENCE 1 RAUTHORS Comynebacterineae; Corynebacteriaceae; Corynebacterium. ITILE Nucleotide sequences coding for branched-chain amino acids export proteins, method for isolating them and their use proteins, method for isolating them and their use Patent: Ep 1096010-A 602-MAY-2001; Degussa AG (DE) ; FORSCHUNGSZENTRUM JUELICH GMBH (DE) FEATURES 11271 FORMAL Degussa AG (DE) ; FORSCHUNGSZENTRUM GULLICH GMBH (DE) FORMAL Degussa AG (DE) ; FORSCHUNGSZENTRUM GULLICH GMBH (DE) FORMAL Degussa AG (DE) ; FORSCHUNGSZENTRUM GULLICH GMBH (DE) FORMAL Degussa AG (DE) ; FORSCHUNGSZENTRUM GULLICH GMBH (DE) FORMAL DEGUS ACTION (Qualifiers 11271) FORMAL DEGUS ACTION (Qualifiers 11271)	721 ATCCGGTACTTCTT	641 ATTANGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACCCTTGGATTCCTGC 601 CGAACGAAAAGCAGATCCCTTCTCTCTCTCTCGCAGGTTTGAGCTTTACCATTGCTCTT 701 CGAACGAAAAAGCAGATCCCTTCTCTCTCTCTCGCAGGTTTGAGCTTCACCATTGCTCTT 661 GTGGTAATCCAGGTCAGGCCCTATTTGCGGGCCTGCTGATCTTCTTGGGTCTGGTGACC 6761 GTGGTAATTCCAGGTCAGGCCCTATTTGCGGGCGTGCTGATCTTCTTGGGTCTGTTGACC 67761	A61 AACCCATTGCCCGTTTCTATTCGCGCTTATCGAAGCAAAGCTACGCAGTCACT 520 QY 421 GCGGCCAGGCCCGCAGGCTGGTCGGCGACTTATCTCAATGCAAATAGCGTTTCAC 480	241 ATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCTGGGGGCCATCGCGCTCACCACA 1

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Kennerknecht, N., Sahm, H., Eggeling, L. and Pfefferle, W. Rucleotide sequences coding for the export of branched chain acids, process for the isolation thereof and use thereof Patent: US 6613545-A 1 02-SEP-2003;

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Similarity 100.0%; Pred. No. 1e-184;
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                                      CGAACGAAAAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTT
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DRS Kennerknecht,N., Sahm,H., Eggeling,L. and Pfefferle,W.

Nucleotide sequences coding for the export of branched chain acids, process for the isolation thereof and use thereof Patent: US 6613545-A 6 02-SEP-2003;

RNAL Patent: US 6613545-A 6 02-SEP-2003;

Location/Qualifiers

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GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT GTGCAAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG GTGCAAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG TIGCIGGIGAACTICCGCCACGTATICTATGCGTITTCATICCCGCTGCATGIGGTCAAA GGCTACGAATGGTGGGCACACCGACTGTTTTCCGGGCCTGATTTTCGCGGGCTCCACCGAA GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTTATTCAATAC AACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT AACCCCATTGCCCGTTTCTATTCGGTTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT ATGCTGGTCATCGCCCTCGTTGTGGGCGCCAGCGCCCCTGGGGCGCCATCGCGCTCACCACA ATGCTGGTCATCGCCCTCGTTGTGGGCGCGCAGCGCCCTGGGGCGCCATCGCGCCTCACCACA GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGGCCTGATTTTCGCGGGCTCCACCGAA GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTTGGTCTCTTGGTTATTCAATAC GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAACCTCCCTT TTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA 0 Gaps 520 420 460 360 400 300 340 280 180 220 120 160 60

760 660 700 600 640 540 580 480

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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BD162490
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JOURNAL
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AL PATRICE JP 2002191370-A 289 09-JUL-2002;

KYOWA HAKKO KOGYO CO LTD

OS Corynebacterium glutamicum
PN JP 2002191370-A/289

PD 09-JUL-2002

PT 15-DEC-2000 JP 2000405096
PI SATOSHI NAKAGAWA,HIROSHI MIZOGUCHI, SEIKO ANDO,MIKIO HAYASHI,
PI KEIKO OCHIAI
PI KARUHIKO YOKOI, NAOKO TATEISHI, AKIHIRO SENOO,MASATO IKEDA,AKIO
PI OZAKI
PC C12N1/15,
PC C12N1/15,
PC C12N1/21,C12N1/21,C12N5/10,C12N9/00,C12N9/02,C12P7/40,C12M1/00,
PC C12N1/15,
PC C12P13/08,
PC C12P13/08,
PC C12P19/00,C12P19/34,C12P21/02,C12Q1/37,C12Q1/68,G01N33/53, PC
G01N33/566,G01N33/68,G01N37/00//C12P21/08,(C12N1/21,C12R1:15),
PC (C12N1/21,C12R1:13),(C12N1/21,C12R1:01),(C12P13/08,C12R1:15),
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Novel polynucleotide.
BD162490
BD162490.1 GI:27868248
JP 2002191370-A/289.
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Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochi
Yokoi,H., Tateishi,N., Senoo,A., Ikeda,M. and Ozaki,
Novel polynuclectide
                                                                                                                                                                                                                                                                                                                                             unidentified
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Best Local Sim
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Similarity 100.0%; Pred. No. 9.8e-185;
53; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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REFERENCE
AUTHORS
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Degussa AG (DE) ; FORSCHUNGSZENTRUM JUELICH GMBH (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynabacterium glutamicum
Corynabacterium glutamicum
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynabacterineae; Corynabacteriaceae; Corynabacterium.
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                                                                                                                                                                      AACCCATTGCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT
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/mol_type="unassigned DNA"
/db_xref="taxon:1718"
/note="ATCC14752"
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1 (bases 1 to 753)

1 (bases 1 to 753)

Nucleotide sequence encoding the discharge of branched amino acimethod of isolating the same and utilization thereof patent: JP 2001169788-A 2 26-JUN-2001;

DEGUSSA HUELS AG,FORSCHUNGSZENTRUM JUELICH GMBH

OS COrynebacterium glutamicum ATCC14752

PN JP 2001169788-A/2

PD 26-JUN-2001

PD 26-JUN-2001

PP 24-OCT-2000 JP 2000324315

PR 27-OCT-1999 DE 19951708.8

PR 27-OCT-1999 DE 19951708.8

PR 21-OCTE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, WALTER
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Nucleotide sequence encoding
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                                                             GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC
                                                                                                                             GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAAACCTCCCTT
                                   GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC
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(C12N15/09,C12R1:15),(C12N1/21,C12R1:15),(C12P13/06,C12R1:15),
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larity 100.0%;
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Pred. No. 9.8e-185;
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/mol_type="genomic
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Patent: BP 1108790-A 289 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:1718"
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10226.291 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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SUMMARIES

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ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AR391954	RESULT 1	
acids, process for the isolation thereof and use thereof	Nucleotide sequences coding for the export of branched chain amino	Kennerknecht, N., Sahm, H., Eggeling, L. and Pfefferle, W.	1 (bases 1 to 753)	Unclassified.	Unknown.	Unknown.		AR391954.1 GI:40115725	AR391954	Sequence 2 from patent US 6613545.	AR391954 753 bp DNA linear PAT 18-DEC-2003			

Pred. No.

18

the number of results predicted by chance to have a

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RESULT 15
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FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 13 row: F column: 02
Seq primer: gta aaa cga cgg cca gtg.
Seq primer: gta aaa cga cgg cca gtg.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jantaguriyarat, C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G. Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea Unpublished (2003)
Contact: Rod Wing Arizona Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Guyas sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                       Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
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Biological Sciences West, 448A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 835)
                                                                             /organism="Oryza sativa (japonica cultivar-group)"

(mol type="mrNA"

/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="0SUNEC13F02"
/tissue_type="Teaf"
/dev_stage="3 week"
/lab_host="0H10B"
                     /clone lib="OSJNEc"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
KhoI; 6 hrs after innoculation with Rice Blast (C9240-1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                   ATGCCGCCGGGTGTTCGACCGGATCGCGCACCCGACCTGCCGGCCTGGAACGCGCTGCT 198
                        CCGTTTCTATTCGGTTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACTGCGGC 525
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          AL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
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Plate: LLAM9410 row: k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS0091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACK19D16 of RPC1-98 library from Drosophila melanogaster (fruit
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/tissue type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: N/
Site_2: Sall; Cloned unidirectionally. Primer: Olig/
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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BX361080
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ORIGIN
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Best Local &
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37; Conserv
                                                                                                                                                                                                                                                                                                            Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen.Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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(bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BX361080 1201 bp mRNA linear ES BX361080 Homo sapiens PLACENTA COT 25-NORWALIZED Homo clone CSODI079YN16 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                   Faraday Avenue Genoscope sequence ID : CSODI079DG08NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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EST.
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                /tissue type="PLACENTA COT 25-NORMALIZED" /clone Tib="Homo sapiens PLACENTA COT 25-NORMALIZED" /clone Tib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="Ist strand cDNA was primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR v sites of the pCMVSFORT 6 vector. Library was normalized.
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/clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                       1. .1201
                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                           clone="CSODI079YN16"
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Pred. No.
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15;
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Best Local Matches : Query Match

3.0%; Score 38.6; 1 Similarity 10.5%; Pred. No. 22; 34; Conservative 147; Mismatches

DB 13; 142;

Length 1201; Indels

0

Gaps

COMMENT

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FEATURES
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KEYWORDS
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CNS005NG/c
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Best Local Similarity
Matches 7; Conserv
                                               ORGANISM
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Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Bail: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBB022ZA07FP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                     CNS005NG 995 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACK12604 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                           fly), genomic survey sequence.
ALO60428
ALO60428.1 GI:4943359
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="NEUROBLASTOMA"
/clone_Tib="Homo sapiens NEUROBLASTOMA"
/clone_Type: NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned
the Not I and EoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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/mol_type="mRNA"
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Pred. No. 11;
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Mammalia; Butheria; Primates; Caraniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

B 1 (bases 1 to 859)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope.
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5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGTTGCGATTACAGTGGTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTG 1135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /moi_type="genomic DNA"
/db xref="taxon:7227"
/clone="BACR12604"
/clone lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:11287778
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to 995)
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Pred. No. 12;
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sapiens cDNA clone IMAGE:4149244
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AUTHORS
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VERSION
KEYWORDS
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BU448643/c
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JOURNAL
MEDLINE
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                                                                                                                                                                                                                              Query Match 3.1%;
Best Local Similarity 62.9%;
Matches 61; Conservative
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                                                                                                                               865 TICTCCTGTATTCTCCTTGTTGTCGCAGTATGTGCAG 901
                                                                                                                                                                    270
                                                                                                            210
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1 (bases 1 to 756)

1 (bases 1 to 756)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BU448643 TSEQRBN13 Gallus gallus cDNA clone ChEST191c7 5', mRNA
CNS009WA 787 bp
Drosophila melanogaster genome su
BACR20K04 of RPCI-98 library from
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EST.
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PO Box 88, Manch
Tel: 01612008930
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                                                                                                             TTTTGCTAAGGTCACCTTCTTGCTGCAGCCTCTGCAG 174
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                                                                                                                                                                                                                                                                                     01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simon. Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Gallus gallus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="ChEST191c7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _stage="adult"
                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                Score 39.4; DB Pred. No. 11; 0; Mismatches
   p DNA linear GSS 03-JUN-1999
survey sequence T7 end of BAC #
rom Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                             DB 13;
                                                                                                                                                                                                                                  36;
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                                                                                                                                                                                                                                                               756;
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VERSION
KEYWORDS
                                   REFERENCE
AUTHORS
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BX425603
                                                                                             SOURCE
ORGANISM
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VERSION
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                                                                                                                                                                                      DEFINITION
                                                                                                                            KEYWORDS
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      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76;
                                                                                                                                                      885 bp mRNA linear EST 15-1
EX425603 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CLOBB022ZA07 3-PRIME, mRNA sequence.
    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 885)
1 (bases 1 to 885)
1 i, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNa libraries and normalization
Unpublished (2001)
                                                                                                                                            BX425603.1 GI:30770486
                                                                                                            Homo sapiens (human)
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                        274 AYTTGTTYKTTTTCYACWGGRCCTAAGGGTAAATTTCRTTAATTTTWTTGTTTTAATTT
                                                                                                                                                                                     712 GCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTTGTGGTAATTCC 771
                                                                                                                                                                                                                                                                                                             214 TAATTTCGCCATATGGTTATATCGGATTTTTTTTATTGGTCCGCTGA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 787)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ely), genomic survey sequence.
AL054013
AL054013.1 GI:4935590
GSS.
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                                                        AGGTCAGGCCTATTTGCGGCGCCTGCTGATCTTCTTGGGTCTGTTGA 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/mol_type="genomic_DNA"
/db_xref="taxon:7227"
/clone="BACR20K04"
/clone_lb="RPCI-98"
/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        45.5%;
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Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                76;
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EST 15-MAY-2003

FEATURES

source

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Gaps

0

58 864

GSS 19-JUN-2003

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AJ397466 dkfz426 Gallus
AJ397466
AJ397466.1 GI:7130433
EST.
                                                                                                                                                                                                                                 Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 718)

1 (bases 1 to 718)

1 Plachy, J., Korn, B. and Buerstedde, J.M.

Plachy, J., Korn, B. and Buerstedde, J.M.

A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Madeleine.Douaire@roazhon.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +33 (0) 2.23.48.54.70
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Buerstedde JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AJ397466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTGCTAAGGTCACCTTCTTGCTGCAGCCTCTGCAG 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="adipose tissue, granulosa, multi-tissues,
oviduct, small folicule, utero-vaginal gland"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dkfz426 Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pT7T3D-pac; Clone distribution : AGENAE Resource centre. François FIUMI, François Flumi.inra.fr, INRA, CEA Radiobiologie et Etude du genome (IREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"
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/db_xref="taxon:9031"
/clone="gcab0001b.d.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .692
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/tissue_type="Bursa of Fabricius"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
                                                                                                                                                                   organism="Gallus gallus"
|mol_type="mRNA"
                                                                                      clone="217r1
                                                                                                         db_xref="taxon:9031"
                                                                                                                                                 strain="CB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.1%;
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Pred. No. 10
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1 (bases 1 to 743)

1 (bases 1 to 743)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Unpublished (2002)

Other GSSs: OGUAX55TV
Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive, Rockville, Tel: 301-838-5843
Fax: 301-838-0208
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/clone="zyMBMa0397J14"
/clone_lib="ZM_0.7 7.1.5_KB"
/clone_lib="ZM_0.7 7.1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5
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                                                                                                                                 Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliangelifetech.co
http://fulllength.invitrogen.com/ Invitrogen Corporation 10
Faraday Avenue Genoscope sequence ID: CSODI072CC03NP1.
                                                                                                                                                                                                                                                       Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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BX381961 homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens clone CSODIO72YP05 3-PRIME, mRNA sequence.
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/clōne="CSODIO72YPO5"
/tissue type="plaCENTA COT 25-NORMALIZED"
/clone lib="Domo sapiens plaCENTA COT 25-NORMALIZED"
/note="ist strand cDNA was primed with a NotI-oligo(
                                                   /mol_type="maxon:9606"
/db_xref="taxon:9606"
                                                                          organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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MMNBKCVMKMKMKMCCKKVMMBKMCAKKKK 975
                                            ATCCTTAAGCCCCTACGTGAATCACAATTT 966
                                                                                                                                          CTCCTTGTTGTCGCAGTATGTGCAGTCATTACTTTTGCGCTCCGGGCGGTTCCGTTCTTA
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Klopp,C. and Douaire,M.
Construction and primary characterization
multi-tissue cDNA libraries
Unpublished (2003)
Contact: Douaire M
INRA, UMR INRA-ENSAR Genetique Animale
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Gallus gallus
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BX540413 AGENAE Gallus gallus multi-tissues library (
gallus cDNA clone gcab0001b.d.10 5prim, mRNA sequence
65, rue de Saint-Brieuc, RENNES
Tel: +33 (0) 2.23.48.54.63
                                                                                                                                                                                                 Archosauria; Aves; Neognathae; Phasianinae; Gallus.
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                            BX540413.1 GI:33294986
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rault, F., Le Meuth-Metzinger, V.,
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(gcab) Gallus
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RESULT 2
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Class: NotI site.
                                                                                                                                                     47;
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1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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BX356664 Homo sapiens PLACENTA COT 25 NORWALIZED Homo
clone CSODI015YB03 3-PRIME, mRNA sequence
BX356664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr
Email: segref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO15CA02NP1.
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/note="Tist strand CDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
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|mol type="genomic DNA"
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Best Local Similarity 9.1%; Pred. No. 2.7;
Matches 55; Conservative 238; Mismatches
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                        Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 9106 EVRY cedex - France
BP 191 9106 EVRY cedex - France
BR 191 9106 EVRY cedex - France
Invary was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2866.f
Contact: Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen.com/ URL :
pranaday Avenue Genoscope sequence ID : CSODC022BG066P1.
Location/Qualifiers
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/clone_Iib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-cligo(dT)
/note="1st strand cDNA was primed with a NotI collook was
primer. Five prime end enriched, double-strand cDNA was
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sites of the pCMVSPORT 6 vector. Library was normalized."
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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ALIGNMENTS

RESULT 1 AQ936633 LOCUS REFERENCE AUTHORS ACCESSION VERSION KEYWORDS COMMENT SOURCE ORGANISM DEFINITION TITLE
JOURNAL
MEDLINE
PUBMED Contact: Podowski RM
Center for Genomics Research
Karolinska Institute
17177 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-337983 Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 473)
2abarovsky, E.R., Gizatullin, R., Podowski, R. M., Zabarovska, V. V.,
Xie, L., Muravenko, O. V., Kozyrev, S., Petrenko, L., Skobeleva, N.,
Li, J., Protopopov, A., Kashuba, V., Ernberg, I., Winberg, G. and
Wahlestedt, C., L., Kashuba, V., Ernberg, I., Winberg, G. and AQ936633 HSJ41-905 sequence. AQ936633 20175728 10710430 AQ936633.1 GSS. NotI clones in the analysis of the human genome Nucleic Acids Res. 28 (7), 1635-1639 (2000) Homo sapiens (human) Human NotI clones GI:7213011 473 Homo ğ DNA linear GSS 23-AUG-2000 sapiens genomic, genomic survey

Search Job ti	ઠ	ş	문	Ş	皮
Search completed: April 17, 2004, 20:13:02 Job time : 148.874 secs	866 GTCC 869	829 CTTC 832	806 GCCCACATGACGCCACTGCCGGTGTTGCTGCTGCTGGTGGCTGGTGCCCATCGTGAA 865	769 TCCAGGTCAGGCCCTATTTGCGGGCGCTGCTGATCTTCTTGGGTCTGTTGACCATCCGGTA 828	746 ATAGCCGTTGCCTGCTTGCTGCTGCTGTCTTGCTGTCCCATTGCACCCGTAGTGGT 805

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RESULT 12
US-10-021-698A-716
; Sequence 716, Application US/10021698A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  US-60-548-091-19934
, Sequence 19934, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001506
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                                                                                                                                        ; CRGANISM: Homo sapiens
US-60-548-091-19934
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                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19934
LENGTH: 201
                                                                           Query Match
Best Local Similarity
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Best Local
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SEQ ID NO 716
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APPLICANT: ALLEN, KRISTINA
APPLICANT: PANDIT, SUNIL
TITLE OF INVENTION: NUCLECTIDE AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: 2976-4044US1
CURRENT APPLICATION NUMBER: US/10/021,698A
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/211,749
PRIOR PILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 6160
SOFTWARE: Patentin 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: modified base NAME/KEY: modified base LOCATION: (167286)...(167385) OTHER INFORMATION: a, t, c o
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LOCATION: (88987)..(89086)
OTHER INFORMATION: a, t, c
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ORGANISM: Homo sapiens
                                                                                                                                                                             TYPE: DNA
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342 TGCTGGTCATCGCCCTCGTTGTGGGCGCCACCCCTGGGCGCCATCGCGCTCACCACAT 401
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DUPUIS, JOSEE
DEL MASTRO, RICHARD
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llarity 55.1%;
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                                                        Score 33; DB 7;
Pred. No. 0.63;
1; Mismatches
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Pred. No. 39;
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                                                                                              DB 7;
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                                                            61; Indels
                                                                                                Length 201
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US-60-548-091-19938
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                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS73927_1
US-10-767-701-9054
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9054, Application US/10767701

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5355)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 9054
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CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19938
LENGTH: 201
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
2.6%;
Best Local Similarity 54.0%;
Matches 67; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Sorghum bicolor
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1028
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                      Score 32.8; DB 6; Length 1028; Pred. No. 2.1; 0; Mismatches 57; Indels 0
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Pred. No. 0.63;
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709 AAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTTGTGGGTAAT 768

Query Match
Best Local Similarity
Matches 67; Conser

Conservative

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213 CT 212

422 GT

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Sequence 5686, Application US/60548091
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
FULE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5686
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SEQ ID NO 62
LENGTH: 23490
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CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: US 10/737,082
PRIOR FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 300
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APPLICANT: Beard, Chris
APPLICANT: Burgess, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: Li, Zheng
ITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
ILE REFERENCE: 1657/2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21270 GGAGCTGGGGCCTGGCCTGGTGAGCGGCTATGCGCTGCTGGTGGGGGGCCTCGACT 21329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21210 CTCGGTGCTCTTCCCCCCTGCTGATCTCTGGTTCCACCTTCTGGCTGCTCAGGCTCTGGGA 21269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 CCACGGACGCGACCCTGAGCTTCTTGAGCCGGACGCCGATCCTGGGCCTGGTCCTCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 ACCAGCGCCGACGGCCTGGGGCTCTTCTCCTCCAGCACCTTGTGGATGAGGTACTGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 GIGGGCGCAGCGCCCIGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTTCCGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 CCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burgess, Chris
Gannon, Allison
Harvey, Jeanne
Lechner, John F.
                                                                                                                                                                                                                                                                                                                                                                                                           CGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAAACCCCATTGCCC 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTGGGCGCAGCGCCCTGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTTCCGCCA
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Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33.8; DB 6; Length 23490;
Pred. No. 7;
0; Mismatches 87; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-804-291A-500
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US-09-804-291A-500
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/213,849
PRIOR APPLICATION NUMBER: 60/226,534
PRIOR TILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 60/230,732
PRIOR APPLICATION NUMBER: 60/230,732
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/266,862
PRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-07
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PRIOR FILING DATE: 2001-02-07
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SEQ ID NO 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 500, App
GENERAL INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/188,914
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/192,033
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/198,474
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 100337.54287US
CURRENT APPLICATION NUMBER: US/09/804,291A
CURRENT FILING DATE: 2001-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/199,335
PRIOR FILING DATE: 2000-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 24477
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17663 GCTTCAGGAGCACCCGGCACRATTTCAACTCCATGGCGTTCCCGCTGCTGGGATTCTACC 17722
                                                                                                                                                                                                                                                                                                                                             Match 2.6%; Cocal Similarity 54.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17603 TéCTGGTCATCGGCTCCCTGGTGGCTCGCTGGCTCCTGGGGATTCAGGAGGGYGGYTTCT 17662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         462 ACCCCATTGCC 472
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                                                                                      687 CTTTGG 692
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                                                                                                                                       CAAGCCTCTTAGAACTGATGGTCATCCTCTTGGCCGTTGTGACTCTCATGGTTACTCTGG
                                              recree
                                                                                                                                                                               TGATTCCTTTTGAAATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGA 686
                                                                                                                                                                                                                              ACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGTGGAGCTTGCCTGCTCAGACA 568
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Pred. No. 7.
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Pred. No. 1.4;
0; Mismatches 58;
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361

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-765-790-62

FILE REFERENCE: APPLICANT:

Query Match

Local Similarity

Conservative

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421

RESULT 10 US-60-548-091-5686

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RESULT 6
US-10-100-683-11511
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LENGTH: 3173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11511,
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CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/040,162 PRIOR FILING DATE: 1997-03-07
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PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR FILING DATE: 1997-05-23
PRIOR FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: PS900
CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
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PRIOR APPLICATION NUMBER: US 60/043,576
                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: Rosen, et al.
[TLE OF INVENTION: Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                              APPLICATION NUMBER: US 60/056,845 FILING DATE: 1997-08-22 APPLICATION NUMBER: US 60/043,580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/056,892 FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,599
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APPLICATION NUMBER: US 60/047,601
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APPLICATION NUMBER: US 60/047,632
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                                                                                                                                      FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,599
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                                                         APPLICATION NUMBER: US 60/043,314
                                                                                                                    FILING DATE: 1997-05-23
                                                                             FILING DATE: 1997-08-22
                                                                                            APPLICATION NUMBER: US 60/056,664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 CTGGTCATCGCCCTCGTTGTGGGCGCCAGCGCCCTGGGCGCCATCGCGCTCACCACA 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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               CATION NUMBER: US 60/047,632
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                                     1997-04-11
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1997-05
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Pred. No. 1
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS124346_1 US-10-767-701-744

ORGANISM: Sorghum bicolor

TYPE: DNA ORGANISM: FEATURE:

Sequence 744, Application US/10767701
GEMERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 744

With

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                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS92927_1 US-10-767-701-7545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-10-767-701-7545
RESULT 8
US-10-767-701-744/c
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NUMBER OF SEQ ID NOS: 13468
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11511
LENGTH: 7071
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 7545
LENGTH: 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local Similarity
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Best Local S
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                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
FILE REFERENCE: 38-21(53535)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                              ORGANISM: Sorghum bicolor FEATURE:
                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                         315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  785 CAGCTCCCGGCCCCAGTGGTGGGCTCAGGGCTCCTGGGCCCATGGGTCTCACCACA 841
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                                                                                                       375 CCCTGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTTCCGCCACG 422
                                                                                                                                        91
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62; Conserv
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                                                                    CGCTGGCGTCCCTGGCGTGCAGCCGCGTGCTCGTGCGTCGGCGAGG
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ilarity 57.4%;
Conservative
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                                                                                                                                                                                                         Score 34.4; DB
Pred. No. 0.46;
0; Mismatches
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                                                                                                                                                                                                                                          DB 6; Length 666;
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OF SEQUENCES: 7310

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NAME/KEY: misc feature;
LOCATION: (B) LOCATION 1...768;
SEQUENCE DESCRIPTION: SEQ ID NO: 1266;
US-10-417-884A-1266
US-10-767-701-5263
; Sequence 5263, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
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SEQUENCE CHARACTERISTICS:
LENGTH: 768 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR LING DATE: 17-Apr-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532

FILING DATE: 30-Jun-1998

APPLICATION NUMBER: 60/055,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                       327
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                                                                                                                                                                                                                 212
                                                                                                                                          272
                                                                                                                                                                                                                                                                                                                                                                     92
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OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 100 Beaver Street
                                                                                                                                                                                                                                                     CGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCCTGGGCGCCA 386
                                                                                                                                                                                                                                                                                                                                                                     TCAAAGACACGTTACCTACCGTTTTCGGTTATATCGGTATTGGACTTGCATTTGGTATCG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/417,884A
                                                                                                                                                                              TCGCGCTCACCACATTGCTGGTGAACTTCCG 417
                                                                                                                                                                                                               CTGGTTCTGCCCAATTTATCACAGTCAGCATGCTTGCTAGTCACAGCCCATTGCTTTCCA
                                                                                                                                                                                                                                                                                                                                TGGTTATTCAATACGGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCG 326
                                                                                                                                          TCGTTTTCTCGACCTTTCTAGTCAATTCCCG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39.8; DB 6; Length 768; Pred. No. 0.0075; 0; Mismatches 107; Indels
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NESULT 5 US-10-100-683-983/c

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APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(5353)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 10866

LENGTH. 100.
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TYPE: DNA

TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10866, Application US/10767701 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 ATCGTGGCGACGCCGTTGCTGGTGATCTTCAGCCCCGTGCTGGTGCCGGCGGCCATCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 GCGGGCTCCAACGCAAAATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCCTGGGCGCC
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271
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                                                                                                                                                                                                                        1 Similarity
88; Conserv
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                                                                       GTGGCGGTGGTGTCCCCGCAGTTCTGCGCGCGCTACGTGGTGCCCCTGACGGTGACCAAG 270
                                                                                                           TIGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGGCGCTGCTCA 264
                                   AACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTC 517
                                                                                                                                                ATGGCGGCGCCTACTACGGCGGAGGCCCTGCGCCCACCGGCGCGGCGCCGGCCCCT 210
 AAGGCCATCAGCCTCTCCGACGGCGACTTCACCGTCACCGACGCCAACGGCGCCGTC 327
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Pred. No. 0.2;
0; Mismatches
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Pred. No. 0.52;
0; Mismatches
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pending Patents NA New.*

1: /cgn2_6/ptodata/1/pna/PCT NEW COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06 NEW COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08 NEW COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US08 NEW COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US00_NEW_COMB.seq:*
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1271
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
    DB
US-10-767-701-1084
US-10-1417-884A-1266
US-10-167-701-5263
US-10-767-701-10866
US-10-10-683-1983
US-10-10-683-11511
US-10-767-701-744
US-10-767-701-744
US-10-767-701-5686
US-10-767-701-5686
US-60-548-091-19934
US-10-767-701-23189
US-10-767-701-23189
US-10-775-920-136
US-10-775-920-136
US-10-775-920-136
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
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PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6067
LENGTH: 594
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature; LCCATION: (4187715); OTHER INFORMATION: a, t, US-10-156-761-1
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APPLICANT: OMURA, SATOSHI
APPLICANT: IXEDA, HARUO
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HORIKAWA, HIROSHI
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; TYPE: PRT
; ORGANISM: Homo S
US-10-184-644-80
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US-10-184-644-80/c
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 80
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APPLICANT: Baker, Kevin P.
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Publication No. US20030044930A1
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.3%; Score 41.4; DB 14; Best Local Similarity 13.4%; Pred. No. 0.0073; Matches 45; Conservative 103; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227 CURRENT APPLICATION NUMBER: US/10/184,644 CURRENT FILING DATE: 2002-06-28
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..CM.M.GA...S.SCBSS
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RESULT 12
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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Publication No. US20020197605A1
GENERAL INFORMATION:
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APPLICANT: MIZOGUCHI, HIROS
APPLICANT: ANDO, SEIKO
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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                   APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARDO
APPLICANT: ISKIRA, HARDO
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NOMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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                                                                                                                                                                                                                       Sequence 6067, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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SEQ ID NO 1
LENGTH: 3309400
TYPE: DNA
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Best Local Similarity
   PRIOR APPLICATION NUMBER: JP 2001-204089
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3289489 TCAAAAATAACAAGGATTATTCGCTGCCATTATTCGCGGTGGTATTGGCTCTGGTTTCCG 3289430
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GTTTTGTGGCGCCCGAGCAGATGCTGGTTATCGCTTTGACCACGTACTTTTTGATCCTTC 3289370
                                                                                                                                                                                                                                                                                                       GCCGAACGAAAAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTC 758
                                                                                                                                                                                                                                                                                                                                                                                                                   ATCTAAAAGGCATGGATTTTGCCCTGACCGCGCTGTTTGTGGTGCTGGCGTGGGGAGGCAT 3289490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTCTTTGTCACGCTGACTTTGGATTCCT 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTG 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGTCGGTTTGGGGCTGATTCCGCTGGGTTTGGCCTTTGGGCTGTTGATGGTCCAGACAG 3289910
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SAHM, HERMANN

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Sequence 1, Application US/10134640

Publication No. US20030017555A1

GENERAL INFORMATION:

APPLICANT: Batthe, Brigitte

APPLICANT: Kalinowski, Jorn

APPLICANT: Wockel, Bettina

APPLICANT: Pfefferle, Walter

ITILE OF INVENTION: Nucleatide Sequences Coding for the 1rp Gene

FILE REFERENCE: 99109 BT

FILE REFERENCE: 99109 BT

CURRENT APPLICATION NUMBER: US/10/134,640

CURRENT FILING DATE: Z002-04-30

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1

SEQ ID NO 1
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CURRENT APPLICATION NUMBER: US/10/608,504

CURRENT FILING DATE: 2003-06-30

PRIOR APPLICATION NUMBER: US 9/471,803

PRIOR APPLICATION NUMBER: US 9/471,803

PRIOR APPLICATION NUMBER: DE 19951708.8

PRIOR FILING DATE: 1999-12-23

PRIOR FILING DATE: 1999-10-27

NUMBER OF SEQ ID NOS: 12

SOPTWARE: Patentin Ver. 2.1
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APPLICANT:
APPLICANT:
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NAME/KEY: CDS
LOCATION: (1)..(324)
OTHER INFORMATION: brnE
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ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: ATCC14752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 25.5%; Score 324; DB 15; Length 324; Local Similarity 100.0%; Pred. No. 4.3e-99; nes 324; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1033 AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGGATTACAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              853 ATGACAACTGATTTCTCCTGTATTCTCCCTTGTTGTCGCAGTATGTGCAGTCATTACTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTGTTGGACTGGTGAATCTTTTC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTGTTGGACTGGTGAATCTTTTC 1176
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; PEATURE:
; NAME/KEY: -35 signal
; LOCATION: (62)..(67)
; OTHER INFORMATION:
US-10-134-640-1
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US-09-738-626-3408
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                                                       US-09-738-626-3408
                                                                                                                                               TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PRICING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VEY: 3.0
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Best Local Similarity
                                                                                                              SOFTWARE: PatentIn ver.
SEQ ID NO 3408
LENGTH: 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3408, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KBY: CDS
LOCATION: (151)..(612)
OTHER INFORMATION: 1rp-Gen
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LOCATION: (88)..(93)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Corynebacterium glutamicum FEATURE:
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                                                                       ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTGGAACCAGATGATAAAGGTTA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                     HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCAACAAAACTACCCGGCAATTGTGTGATGATTGTAGTGTGCAAAAAACGCAAGAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANDO, SEIKO
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; Pred. No. 1.5e-51;
Score 127.4; DB 9; Pred. No. 6.1e-32;
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                  Length 711;
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Query Match Best Local Similarity

10.0%;

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APPLICANT: Kalinowski, Jorn
APPLICANT: Puhler, Alfred
APPLICANT: Mockel, Bettina
APPLICANT: Piefferle, Walter
TITLE OF INVENTION: Nucleotide Sequences Coding for the lrp Gene
FILE REFERENCE: 990109 BT
CURRENT APPLICATION UNMBER: US/10/134,640
CURRENT FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
TYPE: DNY
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Best Local
                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (434)...(778)
OTHER INFORMATION: downstream region of the lrp gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (398)..(433)
OTHER INFORMATION: 3'-region
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LOCATION: (350)..(376)
OTHER_INFORMATION: 5'-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(349)
OTHER INFORMATION: upsream
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LOCATION: (377)..(397)
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                                                                                                                                                                                                                                                                                                                                                       28.8%; Local Similarity 98.9%; les 368; Conservative
                                                                                                                                                                                                                                                                                                    376 AATGGAATCTAGCTTCATATATTGCACAATAGCCTAGTTGAGGTGCGCAAACTGGCAACA
                                                                                                                               196
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                                            309
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                                                                        GTATTGCGTTTGGTCTCTTGGTTATTCAATACGGCTACGAATGGTGGGCAGCCCCACTGT
                                                                                        GTATTGCGTTTGGTCTCTTGGTTATTCAATACGGCTACGAATGGTGGGCAGCCCCACTGT
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                                                                                                                                                                                                                                                                   TTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCG
                                                                                                                               ACGAPATCGCGCAPGGTCTPPAPACCTCCCTTGCTGCPGCPTTGGGCATGTPCCCGPTTG
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Pred. No. 5.2e-113;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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RESULT 9
US-10-608-504-4
; Sequence 4, Application US/10608504
; Publication No. US20040014123A1
; GENERAL INFORMATION:
; APPLICANT: KENNERKNECHT, NICOLE
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APPLICANT: ANDO, SEAN
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN DATE: 2000-08-03
INMBER OF SEQ ID NOS: 7059
SEQ ID NO 290
SEQ ID NO 290
LENGTH: 324
TYPE: DNA
GRANISM: Corynebacterium glutamicum
US-09-738-626-290
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Publication No. US20020197605A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 324; Conserv
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APPLICANT: MIZOGUCHI, HIROS
APPLICANT: ANDO, SEIKO
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; Pred. No. 4.3e-99;
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APPLICANT: KENNERNSCHT, NICOLE
APPLICANT: SAHM, HERWANN
APPLICANT: BEGELING, LOTHAR
APPLICANT: BEGELING, LOTHAR
APPLICANT: BEFFERLE, WALTER
ITILE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: SCALATION AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: ISCLATION THEREOF AND USE THEREOF
TITLE OF INVENTION: ISCLATION THEREOF AND USE THEREOF
TITLE OF INVENTION INVERS: US/10/608,504
CURRENT FALING DATE: 2003-06-30
PRIOR APPLICATION NUMBER: US 09/471,803
PRIOR APPLICATION NUMBER: US 09/471,803
PRIOR APPLICATION NUMBER: US 1999-12-23
PRIOR APPLICATION NUMBER: US 199-10-27
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
LENGTH: 753
TYPE: UNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
OTHER INFORMATION: brnf
FFATURE:
NAME/KEY: CDS
OTHER INFORMATION: brnf
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US-10-608-504-2
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Publication No. US20040014123A1
GENERAL INFORMATION:
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Best Local Simi
Matches 753;
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                         TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA
                                                                   GCGGCCAGGCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC
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   rCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA
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APPLICANT: Bathe, Brigitte
APPLICANT: Kalinowski, Jorn
APPLICANT: Kalinowski, Jorn
APPLICANT: Puhler, Alfred
APPLICANT: Prefferle, Bettina
APPLICANT: Prefferle, Walter
TITLE OF INVENTION: Nucleotide Sequences Coding for
FILE REFERENCE: 990109 BT
CURRENT APPLICATION NUMBER: US/10/134,640
CURRENT FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 9
SOFTMARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 397
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FERATURE:
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US-10-134-640-7/c
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LOCATION: (1)...(397)
OTHER INFORMATION: 1rp part
US-10-134-640-7
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 28.8%;
Best Local Similarity 98.9%;
Matches 368; Conservative
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CAGCGCCCCTGG
                                                                                                       GTATTGCGTTTGGTCTTGGTTATTCAATACGGCTACGAATGGTGGGCAGCCCCACTGT
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                                                                       TTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCG
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RESULT 4

US-09-738-626-289

(US-09-738-626-289)

(Sequence 289, Application US/09738626

(Publication No. US20020197605A1

(GENERAL INFORMATION:
APPLICANT: MAKAGANA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
APPLICANT: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
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APPLICANT: HAYASHI, MIKIRO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VEY: 3.0
SEQ ID NO 1
LENGTH: 3309400
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
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publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
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Publication No. US20040014123A1

GENERAL INFORMATION:
APPLICANT: KENNERWECHT, NICOLE
APPLICANT: SAHM, HERMANN
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ITILE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE TITLE OF INVENTION: SIGCLATION THEREOF AND USE THEREOF

FILE REFERENCE: 7601/80525

CURRENT APPLICATION NUMBER: US/10/608,504

CURRENT FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: US 09/471,803

PRIOR APPLICATION NUMBER: US 09/471,803

PRIOR APPLICATION NUMBER: US 199-10-27

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PRICE 1999-10-27

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 6

LENGTH: 1271
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Best Local Similarity 100.0%; F
Matches 1271; Conservative 0;
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OTHER INFORMATION: brnf
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Copyright (c) 1993 - 2004 Compugen Ltd.
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0-282	US-10-156-761-1	-10-156-761-57	-10-184-634-32	44	-10-063-685-	-634-4	-10-184	10-010-742-2	09-910-689-21	US-09-778-320-211	US-10-140-864-10	-10-140-805-1	-10-141-759	756-1	-10-140-923	-10-137-871-	?	85-	0-141-761-	0-472-	Ļ	-10-123-1		US-10-063-685-100	10-184-634-	US-10-184-644-310	0-184-634-	-10-184-644-
300	e 1,	571	326	326	12,	48,		e 211,	211,	211,		e 10,	e 10,	e 10,	e 10,	Sequence 10, Appl	e 10,	10,	10,	e 10,	10,	e	e 10,	e 100	e 310	e 310	e 346	e 346

ALIGNMENTS

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US-10-608-504-1
US-10-608-504-1
US-10-608-504-1
J Sequence 1, Application US/10608504
Publication No. US20040014123A1
GENERAL INFORMATION:
APPLICANT: KENNERKNECHT, NICOLE
APPLICANT: SAHM, HERMANN
APPLICANT: SEGLING, LOTHAR
APPLICANT: PFEFERLE, WALTER
TITLE OF INVENTION: NUCLESTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: INCLUSION THEREOF AND USE THEREOF
FILE REFERENCE: 7601/80525
CURRENT FILING DATE: 2003-06-30
PRIOR APPLICATION NUMBER: US/10/608,504
CURRENT FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-10-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR PRILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
TYPE: DAN
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: Gene
LOCATION: (853)
COTHER INFORMATION: brnF
FEATURE:
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Page 8

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; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
TYPE: nucleic acid
; STYANDENNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-030-607-12
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Search completed: April 19, 2004, 18:38:21 Job time : 113.018 secs
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                                                                                                                                                                          327 CGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCCTGGGCGCCA 386
                                                                                       350 TGGTGTACACCACAATGGCTGAGCACTTCCCTGACGT 314
                                                                                                                             387 TCGCGCTCACCACATTGCTGGTGAACTTCCGCCACGT 423
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3205
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US-09-252-991A-2761
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2761
LENGTH: 2061
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                                                                                                                                                               Sequence
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Best Local
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                             tent No.
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                                                                     APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS
                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 2.9%;
Local Similarity 58.0%;
                                                       MBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                    1273 TACTTCCTGATCAACCTCGGCGCCGCCCTCGGCCCGCTGATCGGCCTGACTCTCGGCGTC 1332
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                                                                                                                                           12, Application US/09020956
5. 6261562
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 E: SEED and BERRY LLP 6300 Columbia Center,
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1998-02-18
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                                                                         FOR
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701 Fifth Avenue
                                                                         IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
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; MOLECULE TYPE: CDNA US-09-020-956-12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-198
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DCCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. TITLE OF INVENTION: COMPOUN
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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STATE: WA
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TOPOLOGY: linear
                                                                                                                                                                                                                                  ZIP:
                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     12, Application US/09030607
5. 6262245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H: 751 base pairs nucleic acid DEDNESS: single
                                                                                                                                                                                                                                    98104
                                                                                                                                                                                                                                                                                     Seattle
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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 210121.427C3
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                                                                                                                                           Version #1.30
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TITLE OF INVENTION ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: PATCHILD DATE: SEQ ID NO 8976
LENGTH. 7.76
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US-09-621-976-8976/c
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                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8976
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NUMBER OF SEQ ID NOS:
SEQ ID NO 11418
LENGTH: 1086
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Patent No. 6639063
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 77;
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                Query Match
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CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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3.1%; Score 39; DB 4; Le
Local Similarity 12.6%; Pred. No. 0.0086;
18 30; Conservative 112; Mismatches 97;
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APPLICATION NUMBER: US 60/094,190
APPLICATION 1998-07-27
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                                                                                                   242 SAMWRKKWTCWKGRSSWGSRSTGYYAWMYKKSWCTSRKWMYYKKRRKKWRRKCTSTKRT
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3ER: US 60/074,788
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; Pred. No. 0.01:
0; Mismatches
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Sequence 18033, Application US/09621976
Patent NO. 6639063
GENERAL INFORMATION:
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RESULT 12
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Best Local
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CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
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APPLICANT: Giordanc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 474
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                  313
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                                                                                                                                                                                                                                                                                   642 TIAAGGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCTGCC
                                                                                                                                                                                                                                                    133 WKRWYCSSCCMMYTKGGGSMWTTTWMMRRRKKSYKRWTKGKKKKKTTWMMAAMCYTTWRS
                                                                                                                                                                                                                                                                                                                      73
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                                                                                                                                                                                YMMMMRRAAAAKTYYYCNMSKTMCCMACCCMMCCMRRARSCCMRSCMRSCTYMMCYYYY
                                                TCCGGTACTTCTTCGGGAAAGGCTGCTAAATGACAACT 861
                                                                                                                                                TGGTAATTCCAGGTCAGGCCCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACCA
                                                                                                                                                                                                                  GAACGAAAAAGCAGATCCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTTG 761
                                                                                                                  MYKGGRMYWWRGGMWKRMYWMYKKKSMWKGSCMWKRAWWARKTTYYTWAWYYTTYYKR
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Pred. No. 0.045;
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US-09-252-991A-3205/c Sequence 3205, Application US/09252991A Patent No. 6551, Pp. 1997 Patent No. 6551, Pp. 1997 Pp. 19

APPLICANT: Marc J. I TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: 107

107196.136

Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

PSEUDOMONAS

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US-09-10,----
; Sequence 1266, App.....
; Patent No. 6583275
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and TITLE OF INVENTION: NUCLEIC ACID ANI
ENTEROCOCCUS FA
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US-08-232-463-14
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US-09-107-532A-1266
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Best Local Similarity
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                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

PILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arin'ello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1110
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MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1350
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              620
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                                                                                                                                                                                                                                                                                                                                                CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Beaver Street
                                                                                                                                                                                                                                          OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilarity 3.6%; Pred. No. 2e-06; Conservative 221; Mismatches 157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 52.4;
                                                                                                                                                                                                                                                                                                                                                                                                                          and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                       US-09-252-991A-11376
                                                                                                                                               Query Match
Best Local Sim
Matches 77;
                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11376
LENGTH: 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11376, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1266: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...768
SEQUENCE DESCRIPTION: SEQ ID NO: 1266:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 TARARACCTCCCTTGCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCT
                                     369
                                                                                                             309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGTTATTCAATACGGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                     CAGCGCCCCTGGGCGCCATCGCGCTCACCACATTGCTGGTGAACTTCCGCCACGTATTCT 428
                                                                                                     TTTCCGGCCTGATTTTCGCGGGCTCCACCGAAATGCTGGTCATCGCCCTCGTTGTGGGCG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGTTTTCTCGACCTTTCTAGTCAATTCCCG
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GTGCCGGGTTCTTTTCGATCATCTTCACCACCCTCCTCGACCTCGCAGCACCTGCTCT
                                                                           TGTCCGCCATCGTCTTCGCCGGCGCCCCCCAGTTGGTGGCGATCGGCATGCTCAAGGGCG
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                                                                                                                                               3.1%;
llarity 55.0%;
Conservative
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                                                                                                                                               Score 39.2; DB Pred. No. 0.014; D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302
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                                                                                                                                                                                   DB 4; Length 1038;
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429

ATGCGTTTTCATTCCCGCTG 448

APPLICANT:

SAHM, HERMANN

PPLICANT: KENNERKNECHT,

NICOLE

INFORMATION:

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Sequence 3016, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: GARY Breton et. al
ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO F
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO F
CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT TILING DATE: 1200-01-27

PRIOR APPLICATION NUMBER: US/09/117,747

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PRIOR APPLICATION NUMBER: US/09/117,747

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US-09-489-039A-3016
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APPLICANT: PFEFFELLE, WALTER
TITLE OF INVENTION: NUCLECTIBE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 2112/265496/MAS
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT APPLICATION NUMBER: DS 199 51 708.8
PRIOR APPLICATION NUMBER: DS 199 51 708.8
PRIOR APPLICATION NUMBER: US/09/471,803A
CURRENT APPLICATION NUMBER: DS 199 51 708.8
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.1
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LOCATION: (1)..(324)
OTHER INFORMATION: brnE
OTHER INFORMATION: ATCC14752
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US-08-232-463-14
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Best Local :
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMPLECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 2313-0299
ZIP: 2313-0299
ZIP: 2313-0299
ZIP: 2313-029
ZIP: 2513-029
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APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLFOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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Local Similarity 52.2%;
hes 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Alexandria
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                                                                                                                                                                                                                                            TELEFAX:
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Pred. No. 3.4e-09;
0; Mismatches 119;
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US-09-471-803A-2
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                                                                                                                                                              Sequence 2, Application US/09471803A Patent No. 6613545
GENERAL INFORMATION:
APPLICANT: KENNERKNECHT, NICOLE
APPLICANT: SAHM, HERMANN
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
APPLICANT: PERFERLE, WALTER
TITLE OF INVENTION: NUCLECTIDE SEQUENCE CODING FOR THE EXPORT
TITLE OF INVENTION: ISCLATION THEREOF AND USE THEREOF
TITLE OF INVENTION: ISCLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/265496/MAS
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR FILING DATE: 1999-10-27
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TYPE: DNA
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FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(753)
OTHER INFORMATION: brnF
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US-09-471-803A-2
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 2
LENGTH: 753
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Best Local Similarity
Matches 753; Conserv
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                                                                                                CGAACGAAAAAGCAGATCCCTTCTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTT
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RESULT 4 US-09-471-803A-4 ; Sequence 4, Application US/09471803A

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Patent No. 66:3545

GENERAL INFORMATION:
APPLICANT: KENNERKNECHT, NICOLE
APPLICANT: SAHM, HERMANN
APPLICANT: SHAM, HERMANN
APPLICANT: PFEFFERLE, WALTER
TITLE OF INVENTION: NUCLECTIOE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: NUCLECTIOE SEQUENCE CODING FOR THE EXPORT OF
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LOCATION: (101)..(853)
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NAME/KEY: gene
LOCATION: (853)..(1176)
OTHER INFORMATION: brnE
OTHER INFORMATION: ATCC13032
US-09-471-803A-6
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	Sequence 3, Appli	Sequence 3, Appli	•	•	Sequence 5, Appli	-	~	Sequence 1, Appli	Sequence 1, Appli	Sequence 21, Appl	Sequence 13832, A	Sequence 13729, A	•	•	•	Sequence 1307, Ap	771	Sequence 5047, Ap

APPLICANT: KENNERKNECHT, NICOLE APPLICANT: SAHM, HERMANN APPLICANT: EGGELING, LOTHAR APPLICANT: EGGELING, LOTHAR APPLICANT: PERFERLE, WALTER TITLE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF TITLE OF INVENTION: BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF FILE REFERENCE: 21123/265496/MAS CURRENT FILING DATE: 1999-12-23 CURRENT FILING DATE: 1999-12-23 PRIOR APPLICATION NUMBER: DE 199 51 708.8 PRIOR APPLICATION SEQ ID NOS: 12 SOFTWARE: Pateentin Ver. 2.1 SEQ ID NO 1 OTHER INFORMATION: brnF NAME/KEY: gene LOCATION: (853)..(1176) OTHER INFORMATION: brnE OTHER INFORMATION: ATCC14752 US-09-471-803A-1 RESULT 1 US-09-471-803A-1 Sequence 1, Application Patent No. 6613545 GENERAL INFORMATION: NAME/KEY: gene LOCATION: (101) ORGANISM: Corynebacterium glutamicum TYPE: DNA ENGTH: 1271 Application US/09471803A ..(853)

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Search completed: April 19, 2004, 11:42:05 Job time : 593.9 secs

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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium. Coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynuclectides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to corynebacterium glutamicum, polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACA01294
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Best Local S
Matches 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New lrp gene from coryneform bacteria, used to prepare transformants with increased synthesis of amino acids, particularly lysine and isoleucine.
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                                                                                                                                                                                                                                                                                                       Sequence
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                             04-JUN-2003
                                               ACA01968;
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185; Conserv
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                                                                   standard; DNA; 177
                                                                                                                TCGGC 1
                                                                                                                                  TCGGC 185
                                                                                                                                                                      TCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTGGAACCAGATGATAAAGGTTA
                                                                                                                                                                                          TGGCAACAAAACTACCCGGCAATTGTGTGATGATTGTAGTGTGCAAAAAACGCAAGAGAT
                                                                                                                                                                                                           TGGCAACAAAACTACCCGGCAATTGTGTGATGATTGTAGTGTGCAAAAAACGCAAGAGAT
                                                                                                                                                      TCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTGGAACCAGATGATAAAGGTTA
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larity 100.0%;
Conservative (
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88. .93
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/product=
                                                                                                                                                                                                                                                                                                         166 A; 173 C; 178 G; 198 T; 0 U; 0 Other;
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      20-JUN-2001
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glutamicum

derived ORF SEQ

IJ

1959

18-DEC-2000; 2000EP-00127688

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Query Match
Best Local Sim
Matches 177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 647; 709pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid array useful for Corynebacterium glutamicum during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-279970/28.
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                                                                          Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
                                                                                                                                         C glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DEGS ) DEGUSSA AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
EP1108790-A2
                                       Corynebacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGATTGTAGTGTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCA
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                                                                                                                                       coding sequence
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                                       glutamicum
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                                                                                                                                           fragment SEQ ID NO: 3408
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RESULT 11
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Best Local Similarity
Matches 324; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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P-PSDB; AAG90036.
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                                                                                       Corynebacterium
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                                                                                                                                                                                                                                     ACA01970 standard;
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                                                                                                                                                                                                                                                                                                                                                                    GTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTT
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                                                                                                                   nucleic acid array;
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                                                                                                                                               derived ORF SEQ ID 1961.
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                                                                                      glutamicum
                                                                                                                                                                                                                                     DNA;
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                                                                                                                   fermentation;
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, 4.4e-93;
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                                                                                         Fermentation;
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S 밁 Ś 묫 S

밁 Ś B Ś 밁 8 문

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 324 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glutamicum derived polynucleotides described in the disclosure
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                                                                                                                                                                                                                                                                                                                                         GCGCTCCGGGCGGTTCCGTTCTTAATCCTTAAGCCCCTACGTGAATCACAATTTTGTGGGC
TTTGTTGGACTGGTGAATCTTTTC
                                                                            GTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTT
                                                                                                                                                                    AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTG
                                                                                                                                                                                                                                                                   AAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTTCGC
                                                                                                                                                                                                                                                                                                            GCGCTCCGGGCGGTTCCGTTCTTAATCCTTAAGCCCCCTACGTGAATCACAATTTGTGGGC
                                                                                                                                                                                                                                                                                                                                                                                             ATGACAACTGATTTCTCCTGTATTCTCCTTGTTGTCGCAGTATGTGCAGTCATTACTTTT
                                                      GTGGCGCATCTTCGTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTT
                                                                                                                                       AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTG
                                                                                                                                                                                                                           AAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTTCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No. 4.4e-9;
0; Mismatches
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         1176
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TTTGTTGGACTGGTGAATCTTTTC

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standard; DNA; 715 ВP

AAF61688

(first entry)

glutamicum lrp encoding DNA

animal L-amino mal feed acid production; supplement; ds.

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gene;

lysine; isoleucine;

Corynebacterium glutamicum

Key -35_signal Location/Qualifiers 62..67

13-JUN-2001; 2001DE-01028510

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This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) polypeptides; (ii) encodes a polypeptide at least 70% identical with (3) or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least 15 consecutive bases from (i) - (iii). The invention also describes (a) protein derived from sequences of 753 bp (2) or 324 bp (4); (b) coryneform microorganisms, especially Corynebacterium, transformed with
                                                                                                                                                                                                                                         Claim 5;
                                                                                                                                                                                                                                                                                     New export genes from coryneform bacteria, useful for increasing fermentative production of branched-chain amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium
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coryneform bacterium; leucine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. glutamicum brnE DNA.
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DB; AAB86248.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nutrition; ds.
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                                                                                                                                                                                                                                         Page 16; 23pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 brnE; branched-chain amino acid;
isoleucine; valine; medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfefferle
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Best Local S
Matches 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  one or more (I), where these are replicative DNA; (c) production of branched-chain L-aa by fermentation of coryneform bacteria in which the brnE and/or brnF genes (or equivalent sequences) are amplified, especially overexpressed; and (d) method for isolating the brnE and/or brnF genes. (I) is used for transformation of coryneform bacteria being used for fermentative production of branched-chain amino acids, specifically leucine, isolaucine and valine, which are useful in medicine and animal nutrition. (I) can also be used as source of primers and probes for isolation of related sequences. Transformation with (I) increases yield of branched-chain amino acids. This sequence encodes the corynebacterium glutamicum ATCC 14752 brnE protein described in the method of the invention
Coryneform bacterium; amino organic acid synthesis; ds.
                                                     C glutamicum coding sequence fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                            26-SEP-2001
                                                                                                                                                                   AAH65255
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                                                                                                                                                                   standard; DNA; 324
                                                                                                                                                                                                                                                               TTTGTTGGACTGGTGAATCTTTTC
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                     acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 324;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 G; 105 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                             324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.4e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
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RESULT 10
AAH65255
ID AAH65255;
XX
AC AAH65255;
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AC AAH65255;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 290.
XX
Coryneform bacterium; amino acid synthesis; vitamin; sacc
XX
Corynebacterium glutamicum.
XX
Corynebacterium glutamicum.
XX
PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PP 18-DEC-2000; 2000EP-00127688.
XX
PR 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00359162.
PR 07-APR-2000; 2000JP-00379484.
PR 07-APR-2000; 2000JP-00359162.
PR 07-APR-2000; 2000JP-00377484.
PR 07-APR-2000; 2000JP-00380988.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
VA Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
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Yokoi

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                                                                                                                                                      Query Match
Best Local S
Matches 368
                                                                                                                                                                                                                                                 This invention describes a novel isolated nucleic acid (I) from coryneform bacteria used for the fermentative production of selected L-amino acids, by fermenting the amino acid-producing coryneform in which at least the 1rp gene has been weakened or amplified, then isolating amino acids that have accumulated in the medium or cells. (I) is used to transform coryneforms for production of L-amino acids, specifically lysine and isoleucine, which are used in medicine and particularly as animal feed supplement. It may also be used as probes and primers for isolating related sequences. Regulating expression of (I) improves production of amino acids, especially of L-lysine. This sequence encodes a fragment of the Corynebacterium glutamicum 1rp protein which is used in
                                                                                                                                                                                                            Sequence 397 BP; 96 A; 100 C; 104 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 16; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-292927/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-2000; 2000EP-00121159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fermentation; L-amino medicine; animal feed
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New lrp gene from coryneform bacteri
increased synthesis of amino acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DEGS ) DEGUSSA-HUELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glutamicum
                                                                                                                                                                                                                                         method described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          829
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                 129
                                            376
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                                                                                                                                                        368;
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                                                                                                                                                                     Similarity
                                                                                                                   AATGGAATCTAGCTTCATATATTGCACAATAGCCTAGTTGAGGTGCGCAAACTGGCAACA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA; 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCAGGTCAGGCCCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACCATCCGGTA 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCTTCGGGAAAGGCTGCTAAA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCTTCTTGGGAAAGGCTGCTAAA 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCAGGTCAGGCCCTATTTGCGGCGCGCTGCTGATCTTCTTGGGTCTGTTGACCATCCGGTA
GCCTGGAGGTGTCGCCATCCAAGGCAGCCCTGGAACCAGATGATAAAGGTTATCGGCGCT
                                                                  AATGGAATCTAGCTTCATATATTGCACAATAGCCTAGTTGAGGTGCGCAAACTGGCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfefferle W,
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lrp encoding DNA fragment SEQ ID 7
                                                                                                                                                                    28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid production; lrp gene; lysine; isoleucine;
supplement; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Puehler
                                                                                                                                                        0
                                                                                                                                                                 Score 365.6; DB 4;
Pred. No. 2.2e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 bacteria, used to prepare transformants with acids, particularly lysine and isoleucine.
                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kalinowski
                                                                                                                                                                                    DB 4;
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                                                                                                                                                                                 Length
                                                                                                                                                        Indels
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                                                                                                                                                                                    397;
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                                                                                                                                                      Gaps
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                                                                        128
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                   188
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AATGGAATCTAGCTTCATATATTGCACAATAGCCTAGTTGAGGTGCGCAAACTGGCAACA

Matches 368; Query Match Best Local

Similarity

28.8%;

Conservative

0

Score 365.6; DB 4; Pred. No. 3.2e-106; 0; Mismatches 4;

4.

Indels Length

0

Gaps

83

Sequence 778 BP; 175 A; 208 C; 207 G; 188 T; 0 U; 0 Other;

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ARESULT 8
AAP61695/c
ID AAP616
XX AAP616
XX AAP616
XX AAP616
XX Permen
KW Fermen
KW Fermen
KW Fermen
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                                                   amino acids, by fermenting the amino acid-producing coryneform in which at least the lrp gene has been weakened or amplified, then isolating amino acids that have accumulated in the medium or cells. (I) is used to transform coryneforms for production of L-amino acids, specifically lysine and isoleucine, which are used in medicine and particularly as animal feed supplement. It may also be used as probes and primers for isolating related sequences. Regulating expression of (I) improves production of amino acids, especially of L-lysine. This sequence encodes a fragment of the Corynebacterium glutamicum lrp protein which is used in the method described in the invention
                                                                                                                                                                                                                                                                                                                               This invention describes a novel isolated nucleic acid (I) from coryneform bacteria used for the fermentative production of selected L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New lrp gene from coryneform bacteria, used to prepare transformants with increased synthesis of amino acids, particularly lysine and isoleucine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1090993-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fermentation; L-amino acid production; medicine; animal feed supplement; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 17; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moeckel B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 GCCTGGAGGTGTCGCCATCCAAGGCAGCCCTGGAACCAGATGATAAAGGTTATCGGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEGUSSA-HUELS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Puehler A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kalinowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lrp gene; lysine; isoleucine;
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                                                                                                                                                      GCCCGCAGGCTGGTCGGCGACCTTATCTCAATGCAAATAGCGTTTCACTCCTACTG
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                  AAAGCAGATCCCTTCTCGCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTTGTGGTAAT
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This invention describes a novel nucleic acid array involving Corynobacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                     New nucleic acid array useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUN-2001; 2001DE-01028510.
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                                                                                                                                                                                                                                                                      Claim 1; Page 647; 709pp; German.
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FORSCHUNGSZENTRUM JUELICH GMBH
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'nά Mizoguchi H, Senoh A, Ik H, Ando S, Hayashi Ikeda M, Ozaki A; Z ᄌ Ή

WPI; 2001-376931/40. P-PSDB; AAG90035.

Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene gene.

Claim 8; SEQ ID NO 289; 246pp + Sequence Listing; English

The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino analysing

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Matches 1271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-DEC-1999;
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Tateishi
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                                       CGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAAACCCCCATTGCCCGTTTCTA 277208
                                                                   CGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAAAACCCCCATTGCCCGTTTCTA
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Senoh A, Ikeda M, Ozaki A;
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100.0%; P:
1tive 0;
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RESULT AAH211: AAH211: AA XX AC AC AC AC AC AC AC AC AC AC AC AC AC	B 8 B	5 B 6 8	8 8 8 8	용 성· 함 성	8 8 8 8	8 8 8 8	B 8	D 02 D
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0 standard; DNA; 753 BP. 0; 2001 (first entry) amicum brnF DNA. acid production; brnF; brnB; branched-chain amino orm bacterium; leucine; isoleucine; valine; medicin nutrition; ds. accterium glutamicum.		GCACCATCGTTTTTGTTGGACTGGTGAATCTTTTCTAAAACTGCATAAATAA	TCAACGTTTCGCAGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTT	GTCATTACTTTTGCGCTCCGGGCGGTTCCGTTAATCCTTAAGCCCCTACGTGAATCA	CCTATTTGCGGCGTGCTGATCTTCTTGGGTCTGTTGACCATCCGGTACTTCTTCTGGG	CCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCTGCCGAACGAA	TCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAAATTAAGGGCCTCGAGTTCG	
e a cid;		ATARCAAAAAT aTARCAAAAAT	TCATTGCCGTT TCATTGCCGTT GCGTTGGCGCT GCGTTGGCGCT	TACGTGAATCA TACGTGAATCA TTTTGACCGCA	TTCTTCTTGGG	AAGCAGATCCC AAGCAGATCCC CCAGGTCAGGC	CTCGAGTTCGC CTCGAGTTCGC	 cccgcaggcig graffcggcgg
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720 660 660 600 600 540

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960 960 900

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This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that (c) encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) copolypeptides; (ii) encodes a polypeptide at least 70% identical with (3) cor (5); (iii) is the complement of (i) or (ii), or (iv) contains at least cor (5); (iii) is the complement of (i) or (ii), or (iv) contains at least cor (c) is consecutive bases from (1)-(iii). The invention also describes (a) coryneform microorganisms, especially corynebacterium, transformed with contain craby fermentation of coryneform bacteria in which the coryneformhed-chain L-aa by fermentation of coryneform bacteria in which the corynead-chain panels (or equivalent sequences) are amplified, corynead-coryneform bacteria being coryneform bacteria being used for fermentative production of coryneform bacteria being used for fermentative production of parached-chain amino acide, coryneases yield of barached-chain amino acide, which are useful in medicine and animal nutrition. (I) can also be used as source of primers and coryneases yield of barached-chain amino acide. This sequences the corynebacterium glutamicum arcc 13032 brnf and brnE proteins described in the method of the invention
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FORSCHUNGSZENTRUM JUELICH
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CC at least one sequence that (i) is 70% identical with a sequence that CC encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) CC polypeptides; (ii) encodes a polypeptide at least 70% identical with (3) CC or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least CC 15 consecutive bases from (i)-(ii). The invention also describes (a) CC protein derived from sequences of 753 bp (2) or 324 bp (4); (b) CC coryneform microorganisms, especially Corynebacterium, transformed with CC one or more (1), where these are replicative DNA; (c) production of CC branched-chain I-aa by fermentation of coryneform bacteria in which the CC brnE and/or brnP genes (or equivalent sequences) are amplified, and (b brnE and/or brnP genes (or equivalent sequences) are amplified, CC especially overexpressed; and (d) method for isolating the brnE and/or CC used for fermentative production of branched-chain mino acids, completed in triffically leucine, isoleucine and valine, which are useful in medicine CC and animal nutrition. (I) can also be used as source of primers and CC increases yield of branched-chain amino acids. This sequence encodes the CC crynebacterium glutamicum ATCC 14752 brnP and brnE proteins described in CC the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 1271; Best Local Similarity 100.0%; Pred. No. 0; Matches 1271; Conservative 0; Mismatches
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                                   11-OCT-2000; 2000EP-00122057.
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coryneform bacterium; leucine; isoleucine; valine; medicine;
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                                                                               02-MAY-2001.
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ALIGNMENTS

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RESULT 1
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L-amino acid production; brnF; coryneform bacterium; leucine; animal nutrition; ds.
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                                New export genes from coryneform bacteria, useful for increasing fermentative production of branched-chain amino acids.
                                                         WPI; 2001-391595/42.
P-PSDB; AAB86247, AAB86248.
                                                                                                                             27-OCT-1999;
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isoleucine; valine; medicine;
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This invention describes a novel isolated polynucleotide (I) containing

Claim 4 (i); Page 13; 23pp; German.

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69 AAACTACCCGGCAATTGTGTGATGATTGTAGTGTGCAAAAACGCAAGAGATTCATTC	9 ANTGGAATCTAGCTTCATATATTGCACAATAGCCTAGTTGAGGTGCGCAAACTGGCAAAC 68 	Match 28.8%; Score 365.6; DB 6; Length 397; ocal Similarity 98.9%; Pred. No. 2e-89; s 368; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	/organism="Corynebacterium glutamicum" /mol_type="unassigned DNA" /db_xref="taxon:1718" /note="1rp-Teil 1"	Moeckel,B., Nucleotide s Patent: EP 1 Degussa AG (Corynebacterium glutamicum 4 Corynebacterium glutamicum Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.	C AXI37083 397 bp DNA linear PAT 30-MAY-2001 N Sequence 7 from Patent EP1090993. AXI37083.1 GI:14273428	21 ATCCGGTACTTCTTCGGGAAAGGCTGCTAAA 75	1 ATCCGGTACTTCTTCGGGAAAGGCTGCTAAA 853	761 GTGGTAATTCCAGGTCAGGCCCTAFTTGCGGCGCTGCTGATCTTCGTTGGGTCTGTTGACC 820 661 GTGGTAATTCCAGGTCAGGCCCTAFTTGCGGCGCGCTGATCTTTTGGGTCTGTTGACC 720 661 GTGGTAATTCCAGGTCAGCCTAFTTGCGGCCGAGCTTGTTTGGGTCTTTTGACC 720	601 CGAACGAAAAAGCAGATCCCTTCTCTGCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTT 660	701 CGAACGAAAAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTT 760	541 ATTANGGCCTCGAGTTCGCCCTTTGCTCTCTTTGTCACGCTGACTTTGGATTCCTGC 600	81 TCCTACTGGGTATTCGGCGGTCTCACCGGAAGTGGCGATCGCAAGAGTAATTCATTC	81 TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTGCTTTTGAA 6	21	CCGGTTCTATTCGGTTTTCGGCGACTTATCTCAATGCCAATAGCGTTTCAC 58	61 AACCCCATTGCCCGTTTCTATTCGGTTTTTCGCGCCTTATCGAAGCCTACGCAGTCACT	301 Triscrissifiakorricosociacionarrichariscorriroarricosociscoarisissata 360	401 TIGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA 460	241 ATGCTGGTCATCGCCCCGGTGTGTGGGCGCGAGCGCCCCTGGGCGCCATCGCGCTCACCACA 300	341 ATGCTGGTCATCGCCCTCGTTGTGGGGGCGAGAGCGCCCTGGGCGCCATCGCCGCTCACCACA 400	

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27-OCT-1999 DE 19951708.8
NICOLE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, WALTER
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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C12N1/15,
C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12N9/02,C12P7/40,C12P13/PC
C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12N9/02,C12P7/40,C12P13/PC
C12N19/00,C12P19/34,C12P21/02,C12Q1/37,C12Q1/68,G01N33/53, PC
G01N33/566,G01N33/68,G01N37/00//C12P21/08,(C12N1/21,C12R1:15),
PC
G01N33/569,G01N33/68,G01N37/00//C12P21/08,(C12N1/21,C12R1:15),
PC
G1NN31/56,G01N33/68,G01N37/00//C12P21/08,(C12N1/21,C12R1:15),
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G1NN31/56,G01N33/68,G01N37/00//C12P13/08,(C12N1/21,C12R1:15),
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G1NN31/60,G01N33/68,G01N37/00//C12P13/08,(C12N1/21,C12R1:15),
PC
G1NN31/60,G01N33/68,G01N37/00//C12P13/08,(C12N1/21,C12R1:15),
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KYOWA HAKKO KOGYO CO LTD
OS COTYNEBACTETIUM GIUTAMICUM
PN JP 2002191370-A/289
PD 09-JUL-2002
PD 09-JUL-2002
PT 15-DEC-2000 JP 2000405096
PT SATOSHI NAKAGAWA,HIROSHI MIZOGUCHI,SEIKO ANDO,MIKIO HAYASHI,
PI KEIKO CCHIAI,
PI HARUHIKO YOKOI,NAOKO TATEISHI,AKIHIRO SENOO,MASATO IKEDA,AKI
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Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochi
Nakagiwa,S., Tateishi,N., Senoo,A., Ikeda,M. and Ozaki,
Yokoi,H., Tateishi,N., Senoo,A., Ikeda,M. and Ozaki,
Novel polymucleotide
Patent: JP 2002191370-A 289 09-JUL-2002;
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GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGGCCTGATTTTCGCGGGGCTCCACCGAA
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OZAKI
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/mol_type="genomic DNA"
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CDS	AUTHORS TITLE JOURNAL FEATURES SOUICE	SOURCE SOURCE ORGANISM	χο »	Qy 8:	Qy 70	Qy 70	Qy 64	Qy 58	Оу 53 Об 43	Qy 46 Db 36	Qy 40 0b 30	Qy 341 Db 241	Qy 281 Db 181
/organism="Corynebacterium" /mol_type="unassigned DNA" /db xref="taxon:1718" /db xref="taxon:1718" /note="nATCC14752" 1>753 /note="unnamed protein product; brnF" /codon.start=1 /trans1_table=11 /trans1_table=11 /protein_id="CAC39925.1" /db xref="REWIREMBL:CAC39925" /db xref="REWIREMBL:CAC39925" /trans1ation="MQKTOSIHSSIEVSPSKAALEPDDKGYRRYEIAQGLKTSLAAGL /trans1ation="MQKTOSIHSSIEVSPSKAALEPDDKGYRRYEIAQGLKTSLAAGL /gwypigiapgdlviQygygwwaaplpsglifagstemilvialvygaaplgaialtTtll	3 3	Corynebacterium glutamicum Corynebacterium glutamicum Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.	AX137710 753 bp DNA linear PAT 30-MAY-2001 Sequence 2 from Patent EP1096010. AX137710 AX137710.1 GI:14273889	21 ATCCGGTACTTCTTCTTGGGAAAGGCTGCTAAA 853	761 GTGGTAATTCCAGGTCAGGCCCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACC 820 	701 CGAACGAAAAGCAGATCCCTTCTCTGCTGCTGCAGGTTTGAGCTTCACCATTGCTCTT 760 	641 ATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTCTTTGTCACGCTGACTTTGGATTCCTGC 700	581 TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA 640	521 GCGGCCAGGCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC 580	μ μ ≽—≽	ء, ب	ATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCTGGGCGCCATCGCGCTCACCACA	.81 GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGGCCTGATTTTCGCGGGGCTCCACCGAA 340
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Nucleotide sequences coding for the export of branched chain acids, process for the isolation thereof and use thereof patent: US 6613545-A 2 02-SEP-2003;

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ilarity 100.0%; Pred. No. 3.3e-196;
Conservative 0; Mismatches 0;
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Patent: EP 1108790-A 289 20-JUN-2001;
KYOWA HAKO KOGYO CO., LTD. (JP)
Location/Qualifiers
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Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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                                                    GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAACCTCCCTT
                                                                      GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAACCTCCCTT
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/mol_type="unassigned DNA"
/db_xref="taxon:1718"
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100.0%; Prr
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Ikeda, M. and Ozaki, A.
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Corynebacterium glutamicum BrnE
regulator (lrp) genes, complete
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Export of L-isoleucine from Corynebacterium glutamicum: a Export of L-isoleucine from translocator family two-gene-encoded member of a new translocator family J. Bacteriol. 184 (14), 3947-3956 (2002)

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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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Kennerknecht, N., Sahm, H., Yen, M.R., Patek, M.,
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Kennerknecht, N., Egg
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Query Match Best Local Similarity 100.0%; Score 1271; DB 6; Length 349980; Best Local Similarity 100.0%; Pred. No. 0; Matches 1271; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1271; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GCGCGATCAATGGAATCTAGCTTCATATATTGCACAATAGCCTAGTTGAGGTGCGCAAAC 276788 Db 276729 GCGCGATCAATGGAATCTAGCTTCATATATTGTAGTGTGGAAAAAACCAAC 276788 Qy 61 TGGCAACAAAACTACCCGGCAATTGTGTAGTGTGGAAAAAAACGCAAGAGAT 120	AX120085 LOCUS LOCUS LOCUS LOCUS Sequence 1 from Patent EP1108790. ACCESSION AX120085 AX114121 VERSION AX120085 AX114121 VERSION COTYNEDACTERIUM Glutamicum Bacteria, Actinobacteridae, Actinomycetales; COTYNEDACTERIUM Succession, M., Sench, A., Ikeda, M. and Ozaki, A. TITLE JOURNAL FEATURES SOURCE JOURNAL KYOWA HAKKO KOGYO CO., LTD. (JP) FEATURES SOURCE JOURNAL KYOWA HAKKO KOGYO CO., LTD. (JP) Ocation/Qualifiers 1. 349980 /organism="Corynebacterium glutamicum" /molt="Seq 1 to long (3.309.400) split in 11, seq 1 0.000.001 0.349.980 349.980" ORGANISM AX120085 AX1120085 AX114121 AX120085 AX120085 AX120085 AX114121 AX120085 A	OY 841 AAAGGCTGCTDAAATGACAACTGATTTCTCCTTGTTGTCGCAGTATGTGCA 277569 AAAGGCTGCTAAAATGACAACTGATTTCTCCTTGTTGTCGCAGTATGTGCA 900 grcattacttttgcgcctccagacgattcttctcttgttgtcccctacgatcaatca
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TIGR01055:parE_Gneg: DNA topoisomerase IV, B subunit
TIGR01058:parE_Gpos: DNA topoisomerase IV, B subunit
TIGR01059:gyrB: DNA gyrase, B subunit"
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PF00986:DNA gyrase B subunit, carboxyl terminus
PF01751:Toprim domain
PF02518:Histidine kinase-, DNA gyrase B-, phytochrome-1
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ppnveegtmkqivdmtevsvaailswitmggligvregtvfaaffigfevrqmrklyl
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complement (8795. .9466)
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VADKNAESINVPGLGKVYKGYRGKAAKVIEQELPAIGQLIEKNAQ"
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                                                       CGCAGGTTTGAGCTTCACCATTGCTCTTGTGGTAATTCCAGGTCAGGC
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                                                                                                                                                                                                                                                                 Submitted (24-MX-2002) Satoshi Nakagawa, Kyowa Hakko Kogyo Co. Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida, Tokyo 194-853, Japan (E-mail:snakagawa@xanagen.com, Tel:81-44-829-3031, Fax:81-44-813-1651)
This sequence is conducted by collaboration of Kyowa Hakko Kogyo Co. Ltd. And Kitasato University.
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Corynebacterium glutamicum
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Corynebacterium glutamicum ATCC 13032
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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AP005274.1 GI:21
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4766. .5302

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PF02768:DNA polymerase III beta subunit, C-terminal domain
TIGR00663:dnan: DNA polymerase III, beta subunit"
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AUTHORS
TITLE
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Kennerukunehito,N., Sahm,H., Eggering,L. and Pfefferle,W.
Nucleotide sequence encoding the discharge of branched amino acid,
method of isolating the same and utilization thereof

ML Patent: JP 2001169788-A 4 26-JUN-2001;
DEGUSSA HUELS AG, FORSCHUNGSZENTROM JUELICH GMBH
OS COTYNEDACTETIUM GlUTAMICUM ATCC13032

PN 17 2001169788-A/4

PD 20-JUN-2001

PN 27-OCT-2000 JP 2000324315

PF 24-OCT-2000 JP 2000324315

PF 24-OCT-2999 DE 19951708.8

PI NICOLE KENNERUKUNEHITO,HERWANN SAHM,LOTHAR EGGERING,WALTER PI

PFEFFERLE
PC C12N15/09,C07K14/34,C12N1/21,C12P13/06,C12P13/06,C12R1:15),
PC (C12N15/09,C12R1:15),(C12N1/21,C12R1:15),(C12P13/06,C12R1:15),
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JP 2001169788-A/4.
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Nucleotide sequence encoding method of isolating the same
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/mol_type="genomic DNA"
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unclassified.

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Kennerwkunehito,N., Sahm,H., Eggering,L. and Pfefferle,W. Nucleotide sequence encoding the discharge of branched ammethod of isolating the same and utilization thereof patent: JP 2001169788-A 1 26-UN-2001;
DEGUSSA HUBLS AG,FORSCHUNGSZENTRUM JUELICH GMBH OS Corynebacterium glutamicum ATCC14752
                                                                                                  unidentified
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/db_xref="taxon:32644"
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Matches 1271; Conservative 0.
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Degussa AG (DE) ; FORSCHUNGSZENTRUM JUELICH GMBH (DE) LOCALION/Qualifiers
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Degussa AG (DE) ; FORSCHUNGSZENTRUM JUELICH GMBH (DE)
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Rennerknecht, N., Sahm, H., Eggeling, L. and Pfefferle, W. Rennerknecht, N., Sahm, H., Eggeling, L. and Pfefferle, W. Rennerknecht, N., Sahm, H., Eggeling, L. and Pfefferle, W. Rennerknecht, Sequences coding for the export of branched chain acids, process for the isolation thereof and use thereof Patent: US 6613545-A 6 02-SEP-2003;

Location/Qualifiers

1, 1271
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ALIGNMENTS

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LOCUS	AR391953 1271 bp DNA linear PAT 18-DEC-2003	
DEFINITION	Sequence 1 from patent US 6613545.	
ACCESSION	AR391953	
VERSION	AR391953.1 GI:40115724	
KEYWORDS	•	
SOURCE	Unknown.	
ORGANISM	Unknown.	
	Unclassified.	
REFERENCE	1 (bases 1 to 1271)	
AUTHORS	Kennerknecht, N., Sahm, H., Eggeling, L. and Pfefferle, W.	
TITLE	Nucleotide sequences coding for the export of branched chain amino	
	acids, process for the isolation thereof and use thereof	
TOURNAL	Patent: IIS 6613645-A 1 00-6880-0003:	

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RESULT 15
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RA Metcalf W.W., Birren B.;

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Best Local Similarity
Matches 32; Conserv
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Branched chain amino acid transport protein AzlD.
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Methanosarcinales; Methanosarcinaceae; Methanosarcina.
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                                                                                                                                                                                               61 SNAIDLKTLTEGLIAV-AITVVAHL-LGGRRTILLSVGAGTIVFVGLV--NLF 108
61 D--VQWFLAPYGIPELFTIGIVAGLHLMXRNAMLSIFAGTGLYMALVQFNVF 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.6%; Score 82; DB 17; Lilarity 28.6%; Pred. No. 1; Conservative 20; Mismatches 54;
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SPYGLNEIIAVLVVSYIHIV-FKIPVLSIVCGTITYMILI

104

LTFGL---IAVAITVVAHLLGGRRTLLSVGAGTIVFVGLV 105

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DE Hypot
GN LMO14
COS Bacte
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RN [1]
RP SEQUE
RC WEBLI
RA GLASE
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C STRAIN=ATCC 19089 / CB15;

C STRAIN=ATCC 19089 / CB15;

X MEDILINE=21173698; PubMed=11259647;

X MIEDRINE=21173698; PubMed=11259647;

X Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.]

A Nierman W.C., Feldblyum T.V., Laub M.T., Ohta N., Maddock J.R.,

A Potocka I., Nelson W.C., Newton A. Stephens C., Phadke N.D., El:

A DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry:

A Witterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Whi

A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,

Proc. Natl Acad. Sci. U.S.A. 98:4136-4141(2001).

R PIR; D87534; D87534.
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Best Local
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Q9A5Z6;
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                              Q8Y760;
01-MAR-2002
01-MAR-2002
SEQUENCE FROM N.A.

STRAIN-EGD-e / Serovar 1/2a;

MEDLINE-21537279; PubMed=11679669;

MEDLINE-21537279; PubMed=11679669;

Glaser P., Frangeul L., Buchrieser C., Rusniok C.,

Baquero F., Berche P., Bloecker H., Brandt P., Chak

Charbit A., Chetouani F., Couve E., de Daruvar A.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant

Entian K.-D., Fsihi H., Garcia-del Portillo F., Gar
                                                                                                                                                                                                                                                                Listeria monocytogenes.
Bacteria; Firmicutes; E
                                                                                                                                                                                                                                                                                                                        Hypothetical LMO1443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8Y760
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Pfam; PF04932; Wzy_C; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 407 AA; 43683 MW; 49FFEFD4DD2D0E7D CRC64;
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Caulobacteraceae; Caulobacter.
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(TrEMBLrel.
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annotation update)
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     Durant L., I
F., Garrido
                                                     k C., Amend A.,
, Chakraborty T.,
r A., Dehoux P.,
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dock J.R.,
ke N.D., Ely B.,
        Dussurget
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Best Local S
Matches 29
                                                                                                          Query Match
                                                                                                                                  EMBL; AE016755; AAN78524.1; -.
GO; GO:0016021; C:integral to membrane; IE
GO; GO:0006885; P:regulation of pH; IEA.
GO; GO:0006814; P:sodium ion transport; IE
InterPro; IPR004670; NhaA.
TIGRPAMS; TIGR00773; NhaA; 1.
Complete proteome.
SEQUENCE 388 AA; 41397 MW; EBA6173C08B
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Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kuraph
Madueno E., Maitcurnam A., Mata Vicente J., Ng E., Nedjari
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Pu
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
"Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                              STRAIN=O6:H1 / CFT073 / ATCC 700928;

MEDLINE=23388334; PubMede12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch

Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., S

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.,
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01-MAR-2003 (TrEMBLrel. 2
01-JUN-2003 (TrEMBLrel. 2
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Listilist; LMO01443; -.
Hypochetical protein; Complete
SEQUENCE 108 AA; 12053 MW;
                                                                                                                                                                                                                                Proc.
                                                                                                                                                                                                                                          "Extensive mosaic structure revealed by the complete of uropathogenic Escherichia coli."; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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Enterobacteriaceae; Eschei
                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli 06.
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NHAA OR C0024.
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EMBL; AL591979; CAC99521.1; -.
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                                                                                             Local
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                             IAFALGVLALLGSRVPLALKIFL--MALAIIDDLGAIIIIALFYTNDLSMASLGVAAVAI
                                                       ITFALRAVPFLILK-PLRESQFVGKMAMMMPAGILAILTASTFRSNAIDLKTLTFGLIAV
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                                                                                             15.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gammaproteobacteria;
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Pred. No. 0.77
23; Mismatches
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Last annotation update)
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                                                                                            Score 82.5;
Pred. No. 3.
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E6D4BC1E34514BCF CRC64;
                                                                                  Mismatches
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                                                                                                          DB 16;
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Best Local S
Matches 33
                             Q92BR3 PRELIMINARY; [92BR3, Q92BR3]
O1-DEC-2001 (TrEMBLrel. 19, Cre
O1-DEC-2001 (TrEMBLrel. 19, Las
O1-UN-2003 (TrEMBLrel. 24, Las
Hypothetical protein lin1481.
LIN1481.
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01-OCT-2002
01-OCT-2002
01-JUN-2003
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=22391367; PubMed=12503609;

Ludwig M.G., Seuwen K.;

"Characterization of the human adenylyl cyclase gene family:

"Characterization of the human adenylyl cyclase gene family:

gene structure, and tissue distribution of the nine isoforms.

Gene structure, and tissue distribution of the nine isoforms.

J. Recept. Signal Transduct. Res. 22:79-110(2002).

EMBL; AF497515; AAM94372.1;

EMBL; AF497515; AAM94372.1;

GO; GO:0008294; F:calcium/calmodulin-responsive adenylate cyclog.

GO; GO:0008294; F:calcium/calmodulin-responsive adenylate cyclog.
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NON_TER
NON_TER
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SMART; SM00044; CYCc; 2.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
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NON TER
SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O1-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Adenylate cyclase type I (EC 4.6.1.1) (Fragment).
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                 Listeria innocua.
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                                                                                                                                                                                                                                 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITFALRAVPFLILKP---LRESOF---VGKMAMMMPAGILAILTASTFRSNAI----DLK 67
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                                                                                                                                                                                                                                                        VAVCAVITFALRAVPFLILKPLRESQFVGKMAMMPAGILAILTASTFRSNAI----DLK
                                                                                                                                                                            AIGFGLVVAASHLLVTATLVPAKRPRLMRTLGANALLFVG-VNMY
                                                                                                                                                                                                      TLTEGLIAVA--ITVVAHLLGGRRTLL--SVGAGTIVEVGLVNLF 108
                                                                                                                                                                                                                                 LALLFSLTFALLCCFFALGGFARGSAGAAGGFATAEQGVWQLLLV-TFVSYALLFVRSLL
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952 AA;
     Firmicutes;
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ilarity 31.4%;
Conservative 1
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32062 MW;
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        Bacillales;
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Pred.
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Last annotation updat
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Pred. No. 1.4;
B; Mismatches 44; Indels
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                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                          6AB95F1898F466C6 CRC64;
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        Listeriaceae;
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R
Remmel B., Rose M., Schluster T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
Griece 2046.00.0530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7VI97;
01-OCT-2003
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STRAIN=CLIP 11262 /
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[1]
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EMBL; AL596168; CAC96712.1; -.
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                                                                                                                                                                                                                                                                                                                                                    Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P. Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A. Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.; "The complete genome sequence of the carcinogenic bacterium Helicobacter hepaticus."; Roen J. G., Brock, M., Fox J.G.; "Brock Mall. Acad. Sci. U.S.A. 100:7901-7906(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 51449 / 381;
MEDLINE=22709201; PubMed=12810954;
MEDLINE=22709201; PubMed=12810954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter hepaticus,
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete proteome. SEQUENCE 113 AA; 12511 MW; 6D613F77CEB6C90F
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EMBL, APOOS031; BAC702081; --
Hypothetical protein; Complete proteome.
SEQUENCE 102 AA; 10210 MW; 1D803E3D1A40563B
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Sakaki Y., Hattori M., Omura S.;
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Schell M.A., Karmirantzou M., Snel B., Vilanov
Pessi G., Zwahlen M.-C., Desiere F., Bork P.,
Pridmore R.D., Arigoni F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the human gastrointestinal tract."; Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002). EMBL; AE014801; AA025455.1; -.
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Pfam; PF05437; AzlD; 1.
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RESULT Q8PS24

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Best Local
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Branched-chain amino acid transport protein.
AZLD OR MM3263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN-GOE1 / GO1 / ATCC BAA-199 / DSM 3647 / OCM 88;

MEDLINE-22120827; PubMed=12125824;

MEDLINE-22120827; PubMed=12125824;

Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,

Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,

Martinez-Arias R., Henne A., Wiezer A., Boemecke M., Steckel S

Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S

Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus

Fritz H.-J., Gottschalk G.;

"The genome of Methanosarcina mazei: evidence for lateral gene

"The genome of Methanosarcina mazei: evidence for lateral gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              088444;
088444;
01-NOV-1998
01-NOV-1998
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SEQUENCE
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EMBL; AE013585; AAM32959:1;
InterPro; IPR008407; AzlD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota;
Methanosarcinales; Metha
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Archaea; Euryarchaeota; Euryarchaeota orders incertae
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01-NOV-1998 (TrEMBLrel. 08,
01-JUN-2003 (TrEMBLrel. 24,
Adenylyl cyclase type I (EC
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                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Brain;
MEDLINE=98324784; PubMed=9662407;
Abdel-Majid R.M., Leong W.L., Schalkwyk L.C.,
Abdel-Majid R.M., Fine A., Dobson M.J., (
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF05437; AzlD;
                                                                                                                                EMBL, AP053980; AAC29478.1; -. HSSP; P26769; IAB8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                         Neumann
                                                                                                                                                                                                                                              Loss of adenylyl cyclase I activity
          MGI:99677; Adcyl.

GO:0008294; F:calcium/calmodulin-responsive adenylate
GO:0004393; F:guanylate cyclase activity; IEA.
GO:0016829; F:lyase activity; IEA.
GO:0007242; F:intracellular signaling cascade; IEA.
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Biotechnol. 4:453-461(2002)
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%; Pred. No. 0.32;
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
4.6.1.1) (Fragment).
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Sciurognathi; Muridae;
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0.32;
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SEQUENCE FROM N.A.

STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,

Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,

Usuda Y., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,

"The entire genomic sequence of Corynebacterium efficiens YS-314.";

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AP005224; BAC19735.1; -.

InterPro; IPR008407; Azlb.

Piam; PP05437; Azlb; 1.

Piam; PP05437; Azlb; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 116 AA; 12255 MW; 31B0AAE454103417 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genomic sequence of Corynebacterium Submitted (MAY-2002) to the EMBL/GenBank/DDBJ EMBL; AP005283; BAC00476.1; .
InterPro; IPR008407; AzlD.
Pfam; PF05437; AzlD; 1.
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STRAIN=ATCC 13032
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterineae; Corynebacteriaceae; Corynebacterium
NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical membrane protein Cgl3082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium efficiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.7%; Score 130; DB 16; Length 115; 35.0%; Pred. No. 1.6e-05; tive 16; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Best Local :
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Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
EMBL; AE006391; AAX05710.1; -.
PIR; D86826; D86826.
                                                                                                                                                                                    Complete proteome SEQUENCE 108 AA
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae, Lactococcus.
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01-JUN-2003
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                       Local
62 HLGHLPSVNWNNLLASIPTVLAAIL--TKNLL----VIVLVGVFSL
                             62 NAIDIKTLIF-GLIAVAITYVAHLIGGRRTILSVGAGTIVFVGLVNI 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                           2 SSFEFISLTIIGCAIVTWISRVLPFILLKKMSLPQIVVEYLSFVPVVIMSALWISNLFIQ
                                                                                      3 TDFSCILLVVAVCAVITEALRAVPELILKPLRESQFVGKMAMMMPAGILAILTAST-FRS 61
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                                                                                                                                      Similarity
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                                                                                                                                                                                 108 AA; 12024 MW; 9EE4838C1DFCF972 CRC64;
                                                                                                                         Conservative
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                                                                                                                    18.0%; Score 94.5; DB 16; Length 108; 29.9%; Pred. No. 0.054; tive 24; Mismatches 42; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.4%; Score 128.5; DB 16; 30.7%; Pred. No. 2.2e-05;
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Last annotation update)
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RESULT 5
(082XA6 | PRELIMINARY; PRT; 102 AA.

(082XA6; DT 01-UUN-2003 (TYEMBLrel. 24, Created)
DT 01-UUN-2003 (TYEMBLrel. 24, Last sequence update)
DT 01-UUN-2003 (TYEMBLrel. 24, Last annotation update)
DT Hypothetical protein.

Streptomyces avermitilis.
OS Streptomyces avermitilis.
OS Streptomycineae; Streptomycetaceae; Streptomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetales;
OC STRAIN=4A-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RR STRAIN=4A-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RR MEDLINE=2147403; PubMed=11572948;
RA MEDLINE=2147403; PubMed=11572948;
RA Shinose M., Takahashi Y., Hanamoto A., Takahashi C.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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94.55
88.55
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526
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1: sp_archea:*
2: sp_bacteria:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Q8n167 corynebacte
Q8n168 corynebacte
Q8fsw9 corynebacte
Q9cf69 lactococcus
Q82ka6 streptomyce
Q8g3t6 bifidobacte
Q8p824 methanosarc
Q8p8444 mus musculu
Q8nfm5 homo sapian
Q92br3 listeria in
Q7vi97 hellcobacte
Q9a5z6 caulobacter
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Q8y760 listeria mo
Q8tfg1 methanosarc
Q8tkg9 methanosarc
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Q7zu1	Q8uvb	Q9ус04	Q8dvs	Q9knx4	Q86zm8	Q88e	Q89rx2	Q7wb:	Q7wmj7	05041	Qanmo Qanmo	Q8kdv2	Q8dwd1	Q83sı	Q4523	Q98fr	Q8xa63	Cx0z8Q	Q8zjz6	Q9uye	Q8xdt	Q7u948	Q87ef	Q9pee	Q92uw5	Q985a.	Q88Y2	Q81ys
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ALIGNMENTS

Query Match 100.0%; Score 526; DB 16; Length 108; Best Local Similarity 100.0%; Pred. No. 2.7e-45; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps	RT Encoded Member of a New Translocator Family."; RL J. Bacteriol. 184:3947-3956(2002). DR EMBL; AP005274; BAB97652.1; DR EMBL; AF454053; AAM46685.1; DR InterPro; IPR008407; AzlD.	Nakagawa S.; "Complete genomic sequence of Corynel Submitted (MAY-2002) to the EMBL/Genical Corporation of the EMBL/Genical Corporation of the Emple Corporation of the Emp	GN CGL0259 OR BRNE. OS Corynebacterium glutamicum (Brevibacterium flavum). OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; OC Corynebacterineae; Corynebacteriaceae; Corynebacterium. OX NCBI_TaxID=1718; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;	AILN
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MEDLINE=90204555; PubMed=2319602;

Cummings D.J., Michel F., Domenico J.M., McNally K.L.;

TDNA sequence analysis of the mitochondrial ND4L-ND5 gy

from Podospora anserina. Duplication of the ND4L gene of the production of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of the ND4L gene of 
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01-JTU-1993 (Rel. 26, Last annotation update)
01-JTU-1993 (Rel. 26, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.
                  MEDLINE=90291512; PubMed=2357736;
Cummings D.J., McNally K.L., Domenico J.M., Matsuura E.T.;
"The complete DNA sequence of the mitochondrial genome of Podospora anserina.";
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
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                                                                                                                                                    COMPLETE GENOME.
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4 (POTENTIAL)
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S -> N (IN REF. 1).
S -> A (IN REF. 2 AND 4).
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', A3753FB34E452F9A CRC64;
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Best Local S
Matches 28
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PIR; S0913; S0913; NADHub_oxred4.

InterPro; IPR003916; NADHub_oxred5.

InterPro; IPR003916; Oxidored_q1.

InterPro; IPR001750; Oxidored_q1_N.

Pfam; PF00361; oxidored_q1; 1.

Pfam; PF00362; oxidored_q1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE 652 AA;
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PRINTS; PRO1437; NUOXDRDTASE4.
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AA; 72632 MW; 84CA887B75755FE8 CRC64;
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RESULT 14
GTR8_MOUSE
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Pfam; PF00001; 7tm 1; ...

Pfam; PF0001; 7tm 1; ...

PR.NITS; PR00237; GFCRHDDOPSN.

PROSITE; PS00237; GFROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; GFROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; GFROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; GFROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; GFROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; GFROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; GFROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; GFROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; GFROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; GFROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; GFROTEIN_RECEP_F1_2; 1.

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PROSITE; PS50262; GFROTEIN_RECEP_F1_2; T.

PROSITE; PS50262; GFROTEIN_RECEP_F1_2; T.

PROSITE; PS50262; GFROTEIN_RECEP_F1_2; T.

PROSITE; PS50262; GFROTEIN_RECEP_F1_2; T.

PROSITE; PS5026
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or send an email to license@sisb-sib.ch).
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                       GTR8 MOUSE STANDARD; PRT; 477 AA.

GYNTF3; Q9JUT4; Q9JUZ0;

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Solute carrier family 2, facilitated glucose transporter, member (Glucose transporter type 8) (Glucose transporter type 8)

SLC2A8 OR GLUTS OR GLUTX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                   MEDLINE=20138191; PubMed=10671487; Ibberson M.R., Uldry M.A., Thorens B.; Ibberson M.R. of the control of the control of the central nervous system and insulin-sensitive tissues."; J. Biol. Chem. 275:4607-4612(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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MEDLINE=20283667; PubMed=10821868;
Doege H., Schuermann A., Bahrenberg C., Brauers A., Joost H.-G.;
"GLUT8, a novel member of the sugar transport facilitator family with
                                                              TISSUE=Testi
                                                                                SEQUENCE FROM
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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N-LINKED (GLC
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7 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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        MGG; MGG:1866103; Slc2a8.

GO; GO:0005887; C:integral to plasma membrane; IDA.

GO; GO:0005385; F:glucose binding; IDA.

GO; GO:0005355; F:glucose transporter activity; IDA.

GO; GO:0015758; F:glucose transport; IDA.

GO; GO:0015758; F:glucose transport; IDA.

GO; GO:001666; P:response to hypoxia; IDA.

R InterPro; IPR005124; MFS.

R InterPro; IPR005124; MBS.

R InterPro; IPR005829; Sug_transporter.

InterPro; IPR005829; Sug_transporter.

InterPro; IPR005829; Sug_transporter.
                                                                 Transport;
Multigene f
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                              TRANSMEM
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                                                                                                   PROSITE; PS50850; Mrs; ...
PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
PROSITE: PS00217; SUGAR_TRANSPORT; Transmembrane;
                                                                                                                                                                                        Pfam; PF00083; sugar tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
TIGREAMS; TIGR00879; SP; 1.
          TRANSMEM
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family. 26 47 71

25 46 70 91

CYTOPLASMIC (POTENTIAL).

1 (POTENTIAL).

EXTRACELLULAR

2 (POTENTIAL).

(POTENTIAL). (POTENTIAL)

Glycoprotein;

signaling pathway; IDA.

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STRAIN=129; TISSUB=Embryonic carcinoma;
MEDLINB=20319023; PubMed=10860996;
Carayannopoulos M.O., Chi M.M.-Y., Cui Y., Pingsterhaus J.M.,
McKnight R.A., Mueckler M., Devaskar S.U., Moley K.H.;
"GLUTB is a glucose transporter responsible for insulin-stimulated
glucose uptake in the blastocyst.";
Proc. Natl. Acad. Sci. U.S.A. 97:7313-7318(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glucose transport activity.";
J. Biol. Chem. 275:16275-16280(2000).
                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
EMBL; AJ245936; CAB75719.1; -.
EMBL; Y17802; CAB89915.1; -.
EMBL; AP323061; AAP78366.1; -.
EMBL; AJ413951; CAC88690.1; -.
                                                                                                                            entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3T3-L1 adipocytes by glucose.";
Biochem. Biophys. Res. Commun. 288:969-974(2001).
-!-FUNCTION: Insulin-regulated facilitative glucose transporter.
Binds cytochalasin B in a glucose-inhibitable manner. Seems t
a dual-specific sugar transporter as it is inhibitable by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21547794; PubMed=11689004; Scheepers A., Doege H., Joost H.-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   TRANSPORTERS SUBFAMILY.
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RX MEDILINE-22388.57; PubMed=12477932;

RX MEDILINE-22388.57; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,

RA Altschul S.F. Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,

RA Rodriguez S.C., Grimwood J.W., Green E.D., Dickson M.C.,

RA Rodrigues S., Sanchez A.C.,

RA Rodrigues S., Sanchez A.C.,

RA Rodrigues S., Sanchez A.,

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Loetscher M., Amara A., Oberlin E., Brass N., Legler D.F.,
Loetscher P., D'Apuzzo M., Meese E.U., Rousset D., Virelizier
Loetscher P., D'Apuzzo M., Meese E.U., Rousset D., Virelizier
Baggiolini M., Arenzana-Seisdedos F., Moser B.;
"TYMSTR, a putative chemokine receptor selectively expressed
activated T cells, exhibits HIV-1 coreceptor function.";
Curr. Biol. 7:652-660(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "STRL33, A novel
fusion cofactor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liao F., Alkhatib
Farber J.M.;
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MEDLINE=97311099; Pr
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Nature 388:296-300(1997).
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kopatz S.A., Aronstam R.S., Sharma S.V.; "CDNA clones of human proteins involved in signal transc sequenced by the Guthrie cDNA resource center (www.cdna.submitted (JUN-2003) to the EMBL/GenBank/DDBU databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                    EMBL; AF007545; AAB64221.1; -.
EMBL; U73529; AAB61456.1; -.
EMBL; U73531; AAB61457.1; -.
EMBL; Y13248; CAA73698.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    cells.
SIMILARITY: Belongs to
                         AY322543; AAP84356.1; -. BC033584; AAH33584.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel chemokine receptor-like protein, functions as a pfactor for both macrophage-tropic and T cell line-tropic
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                                                                                                                                                                                                                                                                                                                                                                                      family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K.W.C., Sharma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G., Berger E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Legler D.F.,
t D., Virelizier J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mal transduction
(www.cdna.org).";
                                                                                                                                                                                                                                                                                                                            a collaboration
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RESULT 13
CCR6_PANTR
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 Matches
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Best Local
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DOMAIN
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PRINTS; PR00237; GFCRRHODOSN.

PROSITE; PS00237; G PROTEIN RECEP_F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP_F1 2; 1.

G-protein coupled receptor; Transmembrane;
                                                        Brussel A., Pretet J.-L., Girard M., Butor "Sequences and predicted structures of chimg gpris (BOB).";
AIDS Res. Hum. Poternia
                                                                                                                                                                                                                        CCR6 PANTR
Q9TV16;
15-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                    15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (Greceptor bonzo) (G protein-coupled receptor STRL33).
CXCR6 OR BONZO OR STRL33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                         Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                gpr15 (BOB).";
AIDS Res. Hum. Retroviruses 15:1315-1319(1999).
-i- FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.
-i- SUBCELLULAR LOCATION: Integral membrane protein coupled receptors.
-i- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                               NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0005887; C:integral to plasma membrane; GO:0015026; F:coreceptor activity; TAS. GO:0004930; F:G-protein coupled receptor ac GO:0007186; F:G-protein coupled receptor pt GO:0008166; P:viral replication; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      605163;
                                                                                                                                                                                                                                                                                              96
                                                                                                                                                                                                                                                                                                                                      36
                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                             25;
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                              VFGQVMCKSLLGIYTINFYTSMLILTCITV 125
                                                                                                                                                                                                                                                                                                                 LTASTFRSNAIDLKTLTF---GLIAVAITV
                                                                                                                                                                                                                                                                                                                                   CMYLVVEVCGLVGNSLVLVISIFYHKLQSLTDVELVNLPLADLVEVCTLPFWAYAGIHEW
                                                                                                                                                                                                                                                                                                                                                          CILLVVAVCAVITFALRAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                     342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         39280 MW;
                                                                                                                                                                                                                                                                                                                                                                                                 13.3%;
                                                                                                                                                                                                                                                                                                                                                                                       . 88
copyright.
                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR
3 (POTENTIAL).
CYTOPLASMIC (P
                                                                                                                                                                                                                                                                                                                                                                                       Score 70;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 7.3
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC
BY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR
                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                      9FBC025556D1082E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
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   H
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                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                 003506
                                                                                 chimpanzee
                                                                                                                                                                                                                                                                                                                    80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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  produced through
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                                                                                                                                                                                                                                                                                                                                                                               37;
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 342
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                  STRL33
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signalin.
                                                                                                                                                                                             protein-coupled
                                                                                  (Bonzo)
                                                                                                                                                                                                                                                                                                                                                                                16;
    a collaboration
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 11
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Best Local S
Matches 35
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InterPro; IPR005828; Sub_transpo
InterPro; IPR005829; Sug_transpo
InterPro; IPR003663; Sugar_transpo
InterPro; IPR003663; Sugar_transpfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00171; SUCLEMENTS; PR00171; SUCLEMENTS; PRO0179; SP; 1.

TIGREAMS; TIGR00879; SP; 1.

PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.

PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.

PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
SEQUENCE FROM N.A.

MEDLINE=97373958; PubMed=9230441;
Deng H.K., Unutmaz D., Rewalramani V.N., L

"Expression cloning of new receptors used
                                                                                                                                   O18983;

IS-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 36, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

C-X-C chemokine receptor type 6 (CXC-R6) (CXCR-6) (G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
TRANSMEM
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DOMAIN
TRANSMEM
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DOMAIN
                                                                      Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla, Eutheria, Primetes, Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                 CERAE
                                                        NCBI_TaxID=9534;
                                                                                                                     CXCR6 OR BONZO.
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                      CERAE
                                                                                                                                                                                                                                                                                                             273
                                                                                                                                                                                                                                                               332 VVKMVLTIIWLLWLVDLVGRRRILFIGAAGGSLCMWFIG 370
                                                                                                                                                                                                                                                                                     73 LIAVAITVVAHĻ----ĻGGRRTLLSVGA--GTIV--FVG 103
                                                                                                                                                                                                                                                                                                                                                          Similarity
35; Conser
                                                                                                                                                                                                                                                                                                                                   PFLILKPLRESQ---FVGKMA-MWM-PAGILAI--LTASTERSNAID-----LKTLTEG
                                                                                                                                                                                                                                                                                                             PFLSLKQ-RKVQWRFFLGGMLFFWQNGSGINAINYYSPTVFRSIGITGTDTGFLTTGIFG
                                                                                                                                                                                                                                                                                                                                                         13.7%; Score 72; DB 1; Length 537; larity 35.4%; Pred. No. 7.1; Conservative 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153
161
                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               60103 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MFS.
Sub_transporter.
Sug_transporter.
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                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                              12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELULAR (POTENTIAL)
10 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                        9AC63400FCC164F3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                      342 AA
                Littman D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
  by simian and human
                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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                                                                                                                                                                                                                                                                                 CCR6_HUMAN
                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
                                                                                                                               CCRS_HUMAN STANDARD; PRT; 342 AA.

000575;
000574; 000575;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
CC-X-C chemokine receptor type 6 (CXCR-6) (G protein-coupled receptor bonzo) (G protein-coupled receptor STRL33).

CXCR6 OR BONZO OR STRL33 OR TYMSTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunodeficiency viruses.";
Nature 388:296-300(1997).
-!- FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00237; GFCRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane;

DOMAIN 1 32 EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF007859; AAB64225.1; InterPro; IPR000276; GPCR_R
SEQUENCE FROM N.A.
MEDLINE=97373958; PubMed=9230441;
Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
"Expression cloning of new receptors used by simian and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00001; 7tm_1;
                                                                                                  Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POCAT
                                                                                                                                                                                                                                                                                                                                                96 IFGQVMCKTLLGIYTINFYTSMLILTCITV 125
                                                                                                                                                                                                                                                                                                                                                                              54 LTASTERSNAIDLKTLTF --- GLIAVAITV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                                                                                                                                                                                                                                                                                                                                                                                               7 CILLVVAVCAVITFALRAV-------PFLILKPLRESQFVGKMAMMMPAGILAI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               CMYLVVEVCGLVGNSLVLVISIFYHKLQSLTDVFLVNLFLADLVFVCTLPFWAYAGIHEW 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16
342
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69
104
126
144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
A
                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39226 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 70;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
, 6CBFE389C6E5919E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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4 (POTENTI
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7 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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16-OCT-2001 (Rel. 40, Last sequence u
28-FEB-2003 (Rel. 41, Last annotation
Hypothetical protein NMA0420/NMB2020.
NMA0420 OR NMB2020.
                                                                                                                                                                                                                                                                                                                                               STRAIN=22491 / Serogroup A / Serotype 4A;

STRAIN=22491 / Serogroup A / Serotype 4A;

MEDLINE=20222556; PubMed=10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T. Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T. Davies R.M., Davis P. Devlin K., Feltwell T., Hamlin N., F. Davies R.M., Davis P. Devlin K., Feltwell T., Quail M.A., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEIMA
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NCBI_TaxID=65699, 491;
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EMBL; AE002552; AAF42343.1;
FIR; G81014; G81014.
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STRAIN-74-OR33-1A / FGSC 987;

MEDIXINE-89293848; PubMedd=2525625;

Geever R.F., Huiet L., Baum J.A., Tyler B.M., Patel 1

Rutledge B.J., Case M.E., Giles N.H.;

"DNA sequence, organization and regulation of the qa

Neurospora crassa."

J. Mol. Biol. 207:15-34(1989)

J. Mol. Biol. 207:15-34(1989)

-i- SUBCELIJULAR LOCATION: Integral membrane protein.

-i- SIMILARITY: Belongs to the sugar transporter fam.
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                    This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          Neurospora crassa.
Bukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
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Best Local S
Matches 31
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Moelling J., Breton G., Omelchanko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.I., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001)
J. Bacteriol. 183:4823-4838(2001)
J. Bacteriol. 183:4823-4838(2001)
J. Bacteriol. 183:4823-4838(2001)
J. SUNCILULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transport; TRANSMEM
                                                                                                                                                                                                                                                ACRB ECC
P31224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM TRANSMEM
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[1]
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                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Acriflavine resistance protein B.
ACRB OR ACRE OR B0462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
  SEQUENCE FROM N.A.
STRAIN=K12 / W4573;
MEDLINE=94012493; P
                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                      Escherichia coli.
                                                     Xu J., Bertrand K.P.;
"Nucleotide sequence
Submitted (MAY-1993)
                                                                                                                              NCBI_TaxID=562;
                                                                                                       EQUENCE FROM N.A.
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9 31 POTENTIAL.
8 8 POTENTIAL.
107 129 POTENTIAL.
139 161 POTENTIAL.
171 AA; 18440 MW; CC9AAB476CEC8B0C
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    PubMed=8407802;
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23; Mismatches
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                                                        Escherichia coli."; databases.
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Mau B., Shao r.;
"The complete genome sequence science 277:1453-1474(1997).
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Wayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collar between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20381028; PubMed=10920254; Kawabe T., Fujihira E., Yamaguchi A.; "Molecular construction of a multidrug molecular interaction between ACTA and N-terminal signal sequence of ACTA."; J. Biochem. 128:195-200(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95379493; PubMed=7651136;
Ma D., Cook D.N., Alberti M., Pon N.G., Nikaido H.,
"Genes acrA and acrB encode a stress-induced efflux
Escherichia coli.";
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SUBUNIT: INTERACTS WITH ACRA.

-i- SUBCELLULAR LOCATION: Integral membrane protein.

-i- SIMILARITY: BELONGS TO THE ACRB/ACRD/ACRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Microbiol. 16:45-55(1995).
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TRANSMEM
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BCOGene; BCJ1704; acrB.
InterPro; IPR00136; Acrflvin_res.
InterPro; IPR004764; HAE1.
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M94248, AAAA3411.1; -.
EMBL; U00734, AAA67135.1; -.
EMBL; AE000152; AAC73564.1; -.
EMBL; AE0464; AAB40216.1; -.
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PRINTS; PR00702; AC
TIGRFAMS; TIGR0091:
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s; TIGR00915; 2A0602; 1
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CYTOPLASMIC (BY SI
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PERIPLASMIC (BY SI
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PERIPLASMIC (BY SIMILARITY).
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AcrB, and cleavage of t
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and mutational analysis.",

Proc. Natl. Acad. Sci. U.S.A. 94:13414-13419(1997).

Proc. Natl. Acad. Sci. U.S.A. 94:13414-13419(1997).

IF TUNCTION: This is a calmodulin-sensitive adenylyl cyclase. May be involved in regulatory processes in the central nervous system. It involved in regulatory processes in the central nervous system. It involved in regulatory acquisition and learning.

ICANALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.

ICOPACTOR: Binds 2 magnesium ions per subunit (By similarity).

INIXIME REGULATION: Activated by calcium/calmodulin. Inhibited by the G protein beta and gamma subunit complex.

INIXIME Composed of two homologous domains.

INIXIARITY: Belongs to the adenylyl cyclase class-4/guanylyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krupinski J., Coussen F., Bakalyar H.A., Tang W.-J., Feinstein P.G., Orth K., Slaughter C., Reed R.R., Gilman A.G.; "Adenylyl cyclase amino acid sequence: possible channel- or transporter-like structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chu
Mammalia; Eutheria; Cei
Bovidae; Bovinae; Bos.
NCBI TaxID=9913;
                                                                                                                                                                                                                                                                                                                   PIR; A41350; A41350.

PDB; 1AWK; 28-JAN-98.
InterPro; IPRO01054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 2.
SMART; SM00044; CYCC; 2.
SMART; SM00044; CYCC; 2.
PROSITE; PS00452; GUANYLATE_CYCLASES_1; 2.
PROSITE; PS0125; GUANYLATE_CYCLASES_2; 2.
Lyase; CAMP biosynthesis; Transmembrane; Glycoprotein; Repeat; Calmodulin-binding; Metal-binding; Magnesium; 3D-structure.
DOMAIN

1 65
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-98054247; PubMed-9391039;
Liu Y., Ruoho A.E., Rao V.D., Hurley J.H.;
"Catalytic mechanism of the adenylyl and gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89298382; PubMed=2472670;
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                 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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TRPP CLOAB STANDARD; PRT; 171 AA.

ID TRPP CLOAB STANDARD; PRT; 171 AA.

AC Q97D63;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
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        Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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 186
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aigfglvvaashllvtatlvpakkprlwrtlganallflg-vnvy
                                                    TLTFGLIAVA--ITVVAHLLGGRRTLL--SVGAGTIVFVGLVNLF
                                                                          VAVCAVITFALRAVPELILKPLRESQEVGKMAMMPAGILAILTASTERSNAI----DLK
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706
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407
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355
367
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423
434
444
                                                                                                        Conservative
                                                                                                                                                            AA,
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1014
1015
1030
1033
                                                                                                                   14.3%;
                                                                                                                                                            123978 MW;
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                                                                                                      Score 75; DB:
Pred. No. 7.2;
20; Mismatches
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                                                                                                                                                             CC4AlOBCE224DFF3 CRC64;
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                                                                                                         45;
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Best Local S
Matches 27
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EMBL; D90822; BAA15588.1; -.
EMBL; D90823; BAA15590.1; -.
EMBL; AB016761; AAN80653.1; -.
EMBL; AB016767; AAN83034.1; -.
EMBL; AB01693; AAP16929.1; -.
EMBL; AB015167; AAN83034.1; -.
EMBL; AB016983; AAP16929.1; -.
EMBL; AB016983; AAP16929.1; -.
EMBL; AB016983; AAP16929.1; -.
EMBL; AB016983; AAP16929.1; -.
EMBL; AB016983; AAP16929.1; -.
EMBL; AB016983; AAP16929.1; -.
EMBL; AB016983; AAP16929.1; -.
EMBL; AB016983; AAP16929.1; -.
EMBL; AB016983; AAP16929.1; -.
EMBL; AB016983; AAP16929.1; -.
EMBL; AB016983; AAP16929.1; -.
EMBL; AB016983; AAP16929.1; -.
EMBL; AB016983; AAP16929.1; -.
EMBL; AB016982; DBF441.
InterPro; IPR007982; DBF441.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-S. Flexner; STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
MEDLINE=22590274; PubMed=12704152;
Mei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T.";
Infect Immun. 71:2775-2786 (2003).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SUMCILARITY: STRONG, TO H.INFLUENZAE HI1074.
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SPECIES=S.flexner; STRAIN=301 / Serotype 2a;

SPECIES=S.flexner; STRAIN=301 / Serotype 2a;

MEDIXINE=2272406; PubMed=12384590;

MID O., Yuan Z., Xu J., Wang Y., Shan Y., Lu W., Wang J., Liu H., Jin Q., Yang G., Yu H., Qu D., Dong C Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong C Yang J., Yang F., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Shang L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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Nucleic Acids Res.
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84
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                                                                                                                                                                                                                          l Similarity
27; Conserv
                                                                                                                                                                   VAVCAVITFALRAVPFLILKPLRESQFVGKMAMMPAGILAILTASTFRSNAIDLKTLTF
                                                                                                          VAVSILVLIVRVTPLSTFFFWIEKQGLSIGIILTIGVWAPIASGTLPPSTLIHSFLNW
   KSLVAIAVGVIVSWLGGRGVTLMGSQPQLVAGLLVGTVLGVALFRGVPVGPLIAAGLVSL
                                                      -GLIAVAITVVAHLLGGRRTLL---
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71 PO
106 PO
141 PO
15255 MW;
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Pred. No. 0.43
20; Mismatches
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POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
C24E91E1BA51FE93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete
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                                                                                                                                                                                                                                49;
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                                                         ----SVGAGTIVFVGLVNL
                                                                                                                                                                                                                                Indels
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stt J., Stroud
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RESULT 5 YH37_HAEIN

) (ATP pyrophosphate-lyase) cyclase).

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RESULT 6
CYAL BOVIN
ID CYAL BOVIN
STAND
AC p19754;
DT 01-FEB-1991 (Rel. 17
DT 01-FEB-1991 (Rel. 17
DT 10-OCT-2003 (Rel. 42
DE Adenylate cyclase, t
DE (Ca(2+)/calmodulin a
GN ADCY1.
OS Bos taurus (Bovine).
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Matches 21
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P44301;
01-NOV-1995
01-NOV-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; TRANSMEM 7 27
TRANSMEM 37 57
TRANSMEM 63 83
SEQUENCE 109 AA; 124
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MEDLINB=95350630; FubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.D., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;

Whole-genome random sequencing and assembly of Haemophilus influenzae
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Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus.
NCBI TaxID=727;
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HI1737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is no modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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STRAIN=Rd / KW20 /
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PIR; E64041; E64041.
TIGR; HI1737; ---
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE AZLD/HI1737/HP1330 FAMILY.
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(Rel. 32, Last sequence up)
(Rel. 41, Last annotation)
. protein HI1737.
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                                                           17, Created)
17, Last sequence update)
42, Last annotation update)
type I (EC 4.6.1.1) (ATP p
n activated adenylyl cyclase
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57 POTENTIAL.
83 POTENTIAL.
12423 MW; BCC25DB69F5005DF
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Transmembrane;
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27; Mismatches
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MBL outstation -
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YELF S

AC 013879

DT 15-UIL

DT 15-UIL

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DT 28-PEB

DE PUTALLI

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SEQUENCE
                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-97426617; PubMed-9278501;
Blattner F.R., Plunkett G. III, Bloch C.A., Per
Riley M., Collado-Vides J., Glasner J.D., Rode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P76240; 007965; 007967;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence updat.
10-CCT-2003 (Rel. 42, Last annotation upd
Hypothetical protein yeal.
YEAL OR B1789 OR C2194 OR SF1435 OR S1550
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                                                                                                                               "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map."; DNA Res. 3:379-392(1996).
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Escherichia coli 06, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mplete genome sequence of Escherichia coli K-12."; 277:1453-1474(1997).
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SPECIES=E.coli; STRAIN=06:H1 / CFT073 / ATCC 700928; MEDLINE=22388234; PubMed=12471157;

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EMBL; U93876; AAB80902.1; -.
EMBL; Z99117; CAB44611.1; -.
PIR; H69592; H69592.
Subtilist; BG11916; azlD.
InterPro; IPR008407; AzlD.
Pfam; PF05437; AzlD; 1.
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Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler B., Wedler H., Weitzenegger T.,
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Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis."
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- I- FUNCTION: INVOLVED IN BRANCHED-CHAIN AMINO ACID TRANSPORT.
- I- SUBCIBLULAR LOCATION: Integral membrane protein (Potential).
- I- SIMILARITY: BELONGS TO THE AZLD/HI1737/HP1330 FAMILY.
                                                                               Padan E.;
Submitted
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Na(+)/H(+) antiporter 1 (Sodium/proton anti
NHAA OR ANT OR B0019.
Escherichia coli.
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MEDLINE=88273145; PubMed=2839489;

MEDLINE=88273145; PubMed=2839489;

Karpel R., Olami Y., Taglicht D., Schuldiner S., Padan E.;

"Sequencing of the gene ant which affects the Na+/H+ antip

activity in Escherichia coli.";

J. Biol. Chem. 263:10408-10414(1988).
                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae;
NCBI_TaxID=562;
SEQUENCE FROM N.A
STRAIN=K12;
                                                                                                                                     REVISIONS
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MEDLINE=97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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Isono K., Mizobuchi K., Nakata A.;
"Systematic sequencing of the Escherich
the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Science 277:1453-1474(1997).
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InterPro; IPR004670; NhaA; 1.
TIGRFAMS; TIGR00773; NhaA; 1.
Transmembrane; Inner membrane;
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(NhaA) in
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P44301 haemophilus
P19764 bos taurus
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Q97663 clostridium
P31224 escherichia
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submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: C75003
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <KAW>
A;Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50465.1; PID:e151636
A;Experimental source: strain Orsay
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                                                                   Na+/H antiporter [imported] - Escherichia coli (strain 0157:H7, substrain RIMD C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: A99631
R;Hayashi, T; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB1068
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A; Residues: 1-394 < PAR>
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: A99631
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                                                                                                                                                                                                                                                                                                                                                                                                           68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 DFSCILLVVAVCAVITFALRAVPFLILKPLRESOFVGKMAMMMPAGILAILTASTFRSNA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                     TLTEGLIAVAITVVAHLLG-GRRTLLSV---GAGTIVFVGLVN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLIQSACVILSLASDSLLLLIISSIGFGATFMGTTSLVMP---LARQLSAPGNINLLGLV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLVVAVCAVITFALRAVPFLILKPLR-ESQFVGKMAMMMPAGILAILTASTFRSNAIDLK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher. on, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.0%; Score 79; DB 2; Length 394; 26.2%; Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 314;
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                                                                                                                               Han, C.G
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preliminary

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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-388 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB33440.1; PID:g13359473; GSPDB:GN00154
A; Experimental source: strain O157:H7, substrain RIMD 0509952
C; Genetics:
A; Gene: EC50017
A; Gene: EC50017
C; Superfamily: Na+/H+-exchanging protein nhaA
Search completed: April 16, Job time: 10.4234 secs
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Best Local S
Matches 27
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                                                                                                                77 AITVVAHLLGGRRTLLSVGAGTIVFVGLV 105
                                                                                                                                                                                         18 ITFALRAVPFLILK-PLRESQFVGKMAMWMPAGILAILTASTFRSNAIDLKTLTFGLIAV 76
                                                                                                                                                                                                                            1 Similarity
27; Conserv
                                                                                                                                                                                                                          14.9%; Score 78.5; Dilarity 30.3%; Pred. No. 1.9; Conservative 18; Mismatches
                       2004,
                         06:54:26
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                                                                                                                                                                                                                                                                    Length 388;
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R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, August 1997
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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A; Accession: T38034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z98598; PIDN:CAB11241.1; GSPDB:GN00066; SPDB:SPAC1B3.15c
RESULT 11
B90941
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                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-148 <BLAT> A;Experimentes: GB:AE000274; GB:U00096; NID:g1788089; PIDN:AAC74859.1; PID:g1788090; A;Experimental source: strain K-12, substrain MG1655 C;Superfamily: hypothetical protein ytwI
                                                                                                                                                                                                                                                                                                                                                                                                Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E64939
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hypothetical
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Blattner, F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pothetical protein b1789 - Escherichia coli (strain K-12)
Species: Escherichia coli
Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
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Best Local
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                                                                         84
                                                                                                            72
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                                                                                                                                                                                                                15.0%;
1 Similarity 22.5%;
27; Conservation
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                                                                       KSÍVÁLÁVGÝTVSMÍĞGRGVTÍMGSQPQLVAGLLVGTVLGVALFRGÝPVĞPLTAAĞÍVSÍ
                                                                                                                                               VAVSILVLIIVRVTPLSTFFPWIEKQGLSIGIIILTIGVMAPIASGTLPPSTLIHSFLNW
                                                                                                            -GLIAVAITVVAHLLGGRRTLL-----
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ilarity 29.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, fau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
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Pred. No. 2.1;
                                                                                                                                                                                                                                      Score 79; DB 2; Length 148
Pred. No. 0.71;
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hypothetical protein ECs2498 [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: B90941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Hayashi, T.; Makino, K.; Ohnishi, M.;
gasawara, N.; Yasunaga, T.; Kuhara, S.;
DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: ECs2498
C; Superfamily: hypothetical protein ytwI
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A; Residues: 1-48 <HAY>
A; Cross-references: GB: BA000007; PIDN: BAB35921.1; PID: 913361965;
A; Experimental source: strain O157:H7, substrain RIMD 0509952
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A,Reference number: A99629; MUID:21156231; PMID:11258796 A,Accession: B90941
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A;Cross-references: GB:AE005174; NID:g12515826; PIDN:AAG56778.1;
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Groebeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein yeal [imported] - Escherichia coli (strain 0157:H7, su
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       용
na+/ca+ exchanging protein related PAB1029 - Pyrococcus abyssi (strain Orsay) C;Species; Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999 C;Accession: C75003
                                                                                  RESULT
C75003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        iller, L.; Grotbeck, E.J.
Nature 409, 529-533, 2001
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Best Local S
Matches 27
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Best Local
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27; Conserv
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27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GLIAVAITVVAHLLGGRRTLL----
                                                                                                                                                                                                                                                     VAVSILVLIVRVTPLSTFFPWIEXQGLSIGIIILTIGVNAPIASGTLPSSTLIHSFLW
                                                                                                                                                                                                                                                                                             VAVCAVITEALRAVPELILKPLRESOFVGKMAMWMPAGILAILTASTERSNAIDLKTLTF 71
                                                                                                                                                                         -GLIAVAITVVAHLLGGRRTLL---
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larity 22.5%;
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Pred. No.
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Pred. No. 0.71;
20; Mismatches 4
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Potamousis, K.; Ap
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A;Molecule type: DNA
A;Residues: 1-388 «BLAT»
A;Cross-references: GB:AE000112; GB:U00096; NID:g1786192; PIDN:AAC73130.1; PID:g1786201.
A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain; Glaser, G.; Schuldiner, S.; Padan, E.
J. Biol. Chem. 266, 21753-21759, 1991
A;Title: Expression of a sodium proton antiporter (NhaA) in Escherichia coli is induced A;Reference number: A41201; MUID:92042080; PMID:1657980
A;Accession: A41201
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A;Title: The complete genome sequence of E:
A;Reference number: A64720; MUID:97426617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 0 min
c;Superfamily: Na+/H+-exchanging protein nhaA
C;Keywords: sodium transport; transmembrane protein
C;Keywords: sodium transmembrane #status predicted <TM1>
F;12-28/Domain: transmembrane #status predicted <TM2>
F;59-75/Domain: transmembrane #status predicted <TM3:
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A; Residues: 26-988 < YUR>
A; Residues: 26-988 < YUR>
A; Cross-references: EMBL:D10483; NID:g216434; PIDN:BAA01296.1; PID:g216445
A; Cross-references: EMBL:D10483; NID:g216434; PIDN:BAA01296.1; PID:g216445
R; Karpel, R.; Olami, Y.; Taglicht, D.; Schuldiner, S.; Padan, E.
J. Biol. Chem. 263, 10408-10414, 1988
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R;YURA, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Pujita, N.; Isono, K.;
submitted to the EMBL Data Library, December 1992
A;Description: Systematic sequencing of the Escherichia coli genome: analysis of
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conserved hypothetical membrane protein SMb21531 [imported] C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #earror---
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A;Residues: 26-44,'RFTRL',50,'H',52,'KSS',57-388 <KA2:
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A; Accession: $40541
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Best Local S
Matches 27
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;155-171/Domain: transmembrane #status predicted <TM5>
;181-197/Domain: transmembrane #status predicted <TM5>
;181-197/Domain: transmembrane #status predicted <TM7>
;205-221/Domain: transmembrane #status predicted <TM7>
;223-239/Domain: transmembrane #status predicted <TM6>
;233-299/Domain: transmembrane #status predicted <TM10>
;234-270/Domain: transmembrane #status predicted <TM10>
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;Molecule type: DNA
;Residues: 1-28 <KAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITFALRAVPELILK-PLRESOFVGKMAMMMPAGILAILTASTFRSNAIDLKTLTFGLIAV 76
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Pred. No. 0.96
18; Mismatches
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7; PMID:9278503
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    #text_change
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             30-Sep-2001
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A;Gene:

Query Match Best Local Similarity

15.2%;

Score 80; Pred. No.

DB 2;

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A;Residues 1-345 xXRP  
A;Cross-references: GB:AL591985; PIDN:CAC49371.1; PID:g15140857; GSPDB:GN00167  
A;Experimental source: strain 1021, megaplasmid pSymB  
A;Experimental source: strain 1021, megaplasmid pSymB  
A;Experimental source: strain 1021, megaplasmid pSymB  
A;Experimental source: strain 1021, megaplasmid pSymB  
A;Abola, P.; Ampe, F.; Barlc  
Pela, D.; Chain, P.; Cowie, R.W.; Dhiler, A.; Abola, P.; Ampe, F.; Barlc  
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fish  
L; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.  
A;Title: The composite genome of the legume symbiont Sinorhizobium mediloti.  
A;Reference number: A96039; MUID:21368234; pMID:11474104  
A;Contents: annotation  
C;Genetics:
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A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: C95963
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A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A02515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: F82726
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                                                                               A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Marrins, F. A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J., de M.A.; de Roda Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zanderica, R.C.; Palmieri, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zanderica, R.C.; Palmierica, R.C.; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
as.Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frol
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C,Species: Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE003944; GB:AE003849; NID:g9106023; PIDN:AAF83891.1; GSPDB:GN001
A;Experimental source: strain 9a5c
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A;Residues: 1-589 <SIM>
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Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Species: Xylella :
;Date: 18-Aug-2000
Contents: annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 -----NAIDLKTLTFGLIAVAITVVAHLLGGRRTLLSVGAGTIVFVGLVNLF
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24.8%; Pred. No. 1.1;
tive 16; Mismatches
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N.A.; Fisher, R.F.;
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A;Cross-references: GB:AE005176; PID:g12724619;
A;Experimental source: strain IL1403
C;Genetics:
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A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: D86926
                                                                                                                                                                                                                                                                                                                                                                                                          .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entia D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; ok, C.; Schlueter, E.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1617
A;Statue: preliminary
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C;Species: Listeria innocua
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AH1617
C;Accession: AH1617
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
C;Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein yqfC [imported] - Lactococcus lactis subsp. lactis (strain II1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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A; Residues: 1-108 <STO>
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A;Residues: 1-108 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96712.1;
A;Experimental source: strain Clip11262
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Best Local S
Matches 32
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Best Local :
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83
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                                                                                                                                   9 LLVVAVCAVITFALRAVPFLILKPLRESQFVGKMAMMMPAGIL-AILTASTFRSNAIDLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAIDLKTLTF-GLIAVAITVVAHLLGGRRTLLSVGAGTIVFVGLVNL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSFEFISLTIIGCAIVTWISRVLPFILLKKMSLPQIVVEYLSFVPVVIMSALMISNLFIQ
  SINIENLLATLPTIIT-
                                            TLTF-GLIAVAITVVAHLLGGRRTLLSVGAGTIVFVGLVNL 107
                                                                                              LLVILGCGLVTFIPRVLPFIFVRKLQLPSVVIRYLSYVPLCILTALFVQSLLITNENSFP
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                                                                                                                                                                                                           Score 84.5; DB
Pred. No. 0.15;
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Pred. No. 0.
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  AILTKNLMWİVIVĞIISM 101
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Voss, H.; W
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Fsihi, H.
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RESULT

RESULT C64722

Na+/H+-exchanging protein nhaA - Esci N;Alternate names: Na+/H+ antiporter C;Species: Escherichia coli

Escherichia coli

(strain K-12)

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D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
Science 294, 849-852, 2001
A, A, A, A, C.; Schlueter, T.; Simoes, N.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A, Title: Comparative genomics of Listeria species.
A, Reference number: AB1077; MUID:21537279; PMID:11679669
A, A, Ccession: AC1255
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: D87534
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                                                                                                                                                                                                                                                                               C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AC125
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, L.; Dussurget, O.; Entian, K.D.; I
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A;Molecule type: DNA
A;Residues: 1-407 <GTO>
A;Cross-references: GB:AE005673; NID:g13423820; PIDN:AAK24272.1; GSPDB:GN00148
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C;Species: Listeria monocytogenes
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                                                                                    SYTLEVIIGOGLVTEIERVLPEIEVRKLQLPDVVIRYLSYVP---LCILTALEVQSLLIT 61
                                    LKTLTFG----LIAVAITVVAHLLGGRRTLLSVGAGTIVFVGLVNLF 108
                                                                                                                               SCILLVVAVCAVITFALRAVPFLILKPLRESQFVGKMAMMPAGILAILTASTFRSNAID 65
RENSFPGINIENLLASLPTIITAIL -- TKNLMWIVVVGIISMALIRLF
                                                                                                                                                                               Conservative
                                                                                                                                                                                                  15.8%;
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Pred. No. 0.63
20; Mismatches
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Pred. No. 0.21;
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                                                                                                                                                                                                                        Length 108
                                                                                                                                                                                 Indels 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
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Fsini, H
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd

probable Na+/Ca2+-	D71159	001	325	14.1	74	28
rized m	A97344	งผ	171	14.1	74) 26
	S67856	N	379	14.2	74.5	25
nypothetical prote	C97487	N N	1134	14.3	75	2 2 3 2 4 3
conserved hypothet	AC2705	N	923	14.3	75	22
hypothetical prote	F72623	NI	182		រោ (21
giutathione-reguia branched-chain ami	B82056	٦ N	100	14.4	75 76	20
hypothetical prote	T35134	'n	102	•	76	18
cytochrome-c oxida	D48364	NI	235	. 4	77.5	17
Na+/H antiporter,	A85482	N	388	14.	78.5	L
Na+/H antiporter (RADIDA	s K	4 4 4 4 4 4 4	٠,	70 70 70	
na+/ca+ exchanging	C75003	N	314	ייי	79	13
hypothetical prote	F85789	N	148	ū	79	12
hypothetical prote	B90941	N	148	<u>ب</u>	79	11
hymothetical prote	100004	υĸ	1 6 6 8	π υ	70	
ABC transporter AT	F82726	N	589	າ ທ	80	00
conserved hypothet	C95963	N	345	5	80.5	7
Na+/H+-exchanging	C64722	N	388	ហ	81.5	o (
hypothetical prote	AC1255	ν,	108		œ٠	nu m
hypothetical prote	AH1617	ง	108		44 C	·ω
hypothetical prote	D86826	N	108	8	•	N
hai	H69592	μ	110	8	•	ы
Description	ij	B	Length	Query Match	Score	Result
UMMARIES	SUMM			P		
predicted by chance to have a score of the result being printed, total score distribution.	results to the of the	sis/ equa	e number of han or equal by analysis	is th ter t ived	Pred. No. score grea and is der	ec an
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108	.00% .00% .5 summarie	044	ım Match ım Match ng first	Minimum Maximum Listing	cessing:	Post-proce
	0	000	200000	length: length:	DB seq 1 DB seq 1	Minimum Maximum
parameters: 283366	chosen p		atisfying	hits s	number of	Total nu
sidues	91526 re	961	seqs,	283366	••	Searched
	pext 0.5	Gap	0.0,	BLOSUM6 Gapop 1	table:	Scoring
RTLLSVGAGTIVFVGLVNLF 108	ILLVVAVCAVITF	VAV	Ω	1 MITDES		Sequence:
		'n	608-504	US-10-0		Title:
; Search time 8.4234 Seconds (without alignments) 1233.313 Million cell updates/sec	06:51:17		16, 2004,	April :		Run on:
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13.6	13.6	13.6	13.6	13.6	13.6	13.7	13.7	13.8	13.8	13.8	13.9	13.9	14.0	14.0	14.0
395	351	297	286	104	101	537	227	461	461	156	409	405	1049	1049	1049
N	ы	N	ผ	N	N	N	N	N	N	N	N	N	N	N	N
A82827	T44798	A83049	C71059	C97608	AF2830	G31277	G81014	881080	E81862	B84227	F98347	AI2934	G85543	C90693	B36938
conserved hypothet	iron transport mem	hypothetical prote	hypothetical prote		conserved hypothet	quinate transport	conserved hypothet	drug resistance tr	probable integral	ъ.	probable transport	chromate transport	acridine efflux pu	acridine efflux pu	acriflavin resista

No.	Score	% Query Match	% Query Match Length	B	ij	Description		
щ	96.5	18.3	110	۲ ¦	H69592	branched-chain ami		
N	94.5	18.0	108	N	D86826	hypothetical prote		
ω	84.5	16.1	108	N	AH1617			
4.	83.5	15.9	407	ผ	D87534		_	
ر.	83	15.8	108	N	AC1255			
6	81.5	15.5	388	N	C64722			
7	80.5	15.3	345	N	C95963	conserved hypothet		
00	80	15.2	589	N	F82726	ABC transporter AT		
φ	80	15.2	628	N	T38034	probable transport		
10	79	15.0	148	N	至64939	hypothetical prote		
11	79	15.0	148	N	B90941	hypothetical prote		
12	79	15.0	148	N	F85789	hypothetical prote		
13	79	15.0	314	N	C75003	na+/ca+ exchanging		
14	79	15.0	394	N	AB1068	probable membrane	_	
15	78.5	14.9	388	N	A99631	Na+/H antiporter [
16	78.5	14.9	388	N	A85482	Na+/H antiporter,		
17	77.5	14.7	235	N	D48364	cytochrome-c oxida		
18	76	14.4	102	N	T35134	hypothetical prote	9	
19	76	14.4	656	N	B82056	glutathione-regula		
20	75.5	14.4	109	۲	至64041	branched-chain ami		
21	75.5	14.4	182	N	F72623	hypothetical prote		
22	75	14.3	923	N	AC2705	conserved hypothet		
23	75	14.3	923	N	C97487	hypothetical prote		
24	75	14.3	1134	N	A41350	adenylate cyclase		
25	74.5	14.2	379	N	S67856	GumG protein - Xan	_	
26	74	14.1	171	N	A97344	uncharacterized me		
27	74	14.1	324	N	A83940	sugar ABC transpor		
28	74	14.1	325	N	D71159	probable Na+/Ca2+-		
)	;			,	110000	Person to at out to		

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ALIGNMENTS
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branched-chain amino acid transport protein azlD - Bacillus subtilis

C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 28-Jul-2003
C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 28-Jul-2003
C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 28-Jul-2003
C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 28-Jul-2003
C; Date: 10-Sep-1999 #sequence of the Gram-positive bacterin, G.; Azevedo, V.; Berte:
C; Baron, S.; Brouillet, S.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte:
C; Baron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch.
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A.; Authors: Toollger, D.; Fritz, C.; Fujita, M.; Fujita, V.; Fuma, S.; Galizzi, A.; Galle:
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A.; Authors: Talaber, J.; Lace, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A.; Minters, P.; Wipat, A.; Oudega, B.; Park, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.M.; Levine, A.; Sato, T.; Scanlon,
A.; Minters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, F.
A;Authors: Yoshikawa, H.P.; Zamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, F.
A;Accession: M69592
A.;Arthis: nucleic and commerce of the Gram-positive bacterium Bacillus subtilis.
A;Accession: M69592
A.;Arthis: nucleic and commerce of the Gram-positive bacterium Bacillus subtilis.

;Status: nucleic acid sequence not shown; translation not shown; Molecule type: DNA

1-110 <KUN>

A;Cross-references: GB:Z99117; GB:AL009126; NID:g2634966; PIDN:CAB14611.1; PID:g2635115
A;Experimental source: strain 168
R;Belitsky, B.R.; Gustafsson, M.C.U.; Sonenshein, A.L.; von Wachenfeldt, C.
J. Bacteriol. 179, 5448-5457, 1997
A;Title: An Irp-like gene of Bacillus subtilis involved in branched-cháin amino acid tra A;Reference number: Z22837; MUID:97431495; PMID:9287000
A;Accession: T44778

Status: translated from GB/EMBL/DDBJ

A;Cross-references: EMBL:Y11043; NID:g1926275; PIDN:CAA71941.1; PID:g1926282 A;Experimental source: strain 1A1 C;Genetics:

Superfamily: branched-chain amino acid transport protein, AzlD type Keywords: branched-chain amino acid transport; transmembrane protein

Query Match
Best Local Similarity
Matches 31; Conserv Conservative 18.3%; Score 96.5; DB 1; Length 110; 27.2%; Pred. No. 0.0095; ative 28; Mismatches 42; Indels 1: Indels 13; Gaps

밁 Ś 1 MTTDFSCILLVVAVCAVITFALRAVPFLIL---KPL-RESQFVGKWAWMMPAGILAILTA 56 MIMIMIQQMITIAMVVLGIMLTRELPEMIFPSGKETPKYVQYLGKV---LPSAVIGLLVI 57 6

57 STFRSNAIDLKTLTFG---LIAVAITVVAHLLGGRRTLLSVGAGTIVFVGLVNL 107

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중 유 Search completed: April 16, 2004, 07:03:20 Job time : 9.52089 secs 23 VVAYVIAPSEGMGĀIPWIMSEI-----LPVSI---71 FGLIAVAITVVAHLL-----GGRRTLLSVGĀGTĪVFV 102
62 NWLTSFGIĪWTĀNLLISWSĀGGTFĀSYMĪVSĀFTLVFV 99 :| | || --KSLAGSFATLA 61

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92

LSVGAGTIVF-----VGLVNLF 108

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US-60-556-841-2298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C65105_1.pep
US-10-767-701-40503
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                                       S
                                                                                                                                                                                                                                                             ; ORGANISM: Pseudomonas putida KT2440
US-60-556-841-2298
                                                                                                                                                                         Query Match
Best Local S
Matches 30
                                                                                                                                                                                                                                                                                                                     Sequence 2298, Application US/60556841

GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)
CURRENT APPLICATION NUMBER: US/60/556,841
CURRENT FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 12463
SEQ ID NO 2298
LENGTH: 475
TYPE: TERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 40503
LENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40503, Application US/10767701 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.0%; Score 68.5; DB 6; Length 119; Best Local Similarity 30.8%; Pred. No. 0.57; Matches 33; Conservative 15; Mismatches 26; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nuclecic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ. ID NOS: 63128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kovalic,
                                                                                 131 CA--SLLLWSVHFLVLRGIXBAAFINQVTTVAKVVPLLIFVVIAAFAFRADIFTRDIWGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 IIAGIGIÍFFGFGNGGDAIGLSNÍW 187
189 SNPOFGSVLEOVRNMMLVTVFVFIGIEGASVYSGRAORRSDVGKATVIGFLGVLAL 244
                                            67
                                                                                                           15 CAVITFALRAVPFLILKPLRESQFVGK---MAMMMPAGILAILTASTFRSNAI-----DL
|| : | :| ||:| : : | : | : | : : | | : : |
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                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTLTFGLI-----AVAITVV-----AHLLGGRRTLLS-VGAGTIV-FVGLVNL 107
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       David K.
                                                                                                                                                                       13.0%; Score 68.5; DB 7; Length 475;
25.9%; Pred. No. 2.9;
tive 24; Mismatches 37; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Indels 33;
                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                            Gaps
                                                                                        188
                                                                                                                                  66
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US-10-779-543-23512 ; Sequence 23512, Application US/10779543 ; GENERAL INFORMATION: ; APPLICANT: Williams et al

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11 VVAVCAVITFALRAVPFLILKPLRESQFVGKMAMWMPAGILAILTASTFRSNAIDLKTLT 70

Local Similarity es 26; Conserv

15/

Mismatches

Indels

.74;

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CURRENT APPLICATION NUMBER: US/10/779,543

CURRENT APPLICATION NUMBER: US/10/779,543

CURRENT APPLICATION NUMBER: US/20/20-212

PRIOR APPLICATION NUMBER: 10/076,555

PRIOR APPLICATION NUMBER: 10/076,555

PRIOR APPLICATION NUMBER: 09/217,471

PRIOR APPLICATION NUMBER: 09/217,471

PRIOR APPLICATION NUMBER: 09/217,471

PRIOR APPLICATION NUMBER: 09/08,755

PRIOR APPLICATION NUMBER: 60/08,755

PRIOR APPLICATION NUMBER: 60/08,755

PRIOR FILING DATE: 199-12-23

PRIOR FILING DATE: 199-01-29

PRIOR FILING DATE: 1990-04-40

PRIOR APPLICATION NUMBER: 09/297,648

PRIOR APPLICATION NUMBER: 09/297,648

PRIOR APPLICATION NUMBER: 09/075,234

PRIOR FILING DATE: 1990-01-28

PRIOR APPLICATION NUMBER: 60/072,910

PRIOR APPLICATION NUMBER: 60/075,954

PRIOR APPLICATION NUMBER: 60/075,954

PRIOR APPLICATION NUMBER: 60/080,114

PRIOR APPLICATION NUMBER: 60/080,114

PRIOR APPLICATION NUMBER: 60/080,114

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PRIOR APPLICATION NUMBER: 60/080,114

PRIOR APPLICA
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                                                                                                                                   , OTHER INFORMATION: Clone ID: SORBI-28MAY03-C71332_1.pep
US-10-767-701-43433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-10-767-701-43433
                                                                                                                                                                                                                                                                                                                          Sequence 43433 Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 43433
LEMERAL 110
Query Match
Best Local S
Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                     TYPE: PRT ORGANISM: Sorghum bicolor FEATURE:
                                                                                                                                                                                                                                                                                                               LENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 VNL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 VLKSVGFQSNEAASLASTGVGVVKVISTIPATLLVDHVGSKTFLCIGSSVMAASLVTMGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 VNL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 ILTASTFRSN-AIDLKTLTEGLIAVAITVVAHLL---GGRRTLLSVG----AGTIVEVGL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.9%;
ilarity 34.9%;
Conservative 1:
                             12.8%;
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Pred. No. 3.8;
13; Mismatches
                                Score 67.5;
Pred. No. 0.
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                                                                     Length 119;
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Wendy S. Halsey

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; ORGANISM: HOMO SAPIENS
US-10-667-762-76
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/10/407,386
PRIOR FILING DATE: 2003-04-04
PRIOR PRIOR DATE: 2002-10-21
PRIOR FILING DATE: 2002-10-21
PRIOR PRIOR APPLICATION NUMBER: US/10/125,749
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US/09/988,922
PRIOR FILING DATE: 2001-11-19
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                                US-10-787-018-9
                                                   RESULT 10
                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: F
SEQ ID NO 76
Sequence 9, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/667,762
CURRENT FILING DATE: 2003-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN G PROTEIN-COUPLED RECEPTOR TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FILE REFERENCE: GP-70775B-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT
                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                      36
                                                                                                    96 VFGQVMCKSLLGIYTINFYTSMLILTCITV 125
                                                                                                                                 54 LTASTFRSNAIDLKTLTF---GLIAVAITY 80
                                                                                                                                                                                                                                        25;
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                                                                                                                                                                                                                                                                                                                                                                                               FastSEQ
                                                                                                                                                                  CMYLVVEVCGLVGNSLVLVISIEVHKLQSLTDVELVNLPLADLVEVCTLPEWAYAGIHEW 95
                                                                                                                                                                                                       Manhanandeeshwar Gattı
John W. Quillen, Jr.
Erin M. Toland
Steven Michael Foord
                  Application US/10787018
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George H. Poste
Michel Louis Souchet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bernard Emile Joseph Gout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Philippe Laurent Robert
Stephane Clement Krief
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Henry Sarau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catherine E. Ellis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    David Malcolm Duckworth
Jeffrey Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Menelas N. Pang
Melanie Robbins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Derk J. Bergsma
Nabil A. Elshourbagy
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Philip Graham Szekeres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Han Ngoc Trinh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alexander Taylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isa Vawter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ankaj Agarwal
kandall Forrest Smith
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                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               for Windows Version 3.0
                                                                                                                                                                                                                                                        13.3%;
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                                                                                                                                                                                                                                                        Score 70; DB 6; Length 342; Pred. No. 1.3;
                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                         37;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                         Gaps
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APPLICANT: Gosling, Jennifa APPLICANT: Dairaghi, Danie

Dairaghi, Daniel J Hanley, Michael

Query Match 13.1%; Score 69; DB Best Local Similarity 22.1%; Pred. No. 2.4; Matches 32; Conservative 24; Mismatches

DB 7;

Length 462;

45;

Indels

44;

Gaps

-QFVGKMA------MWMPAG 49

103 MSEIIAVGSYTKYWFPDLPAWIPGIVAMVILGAANLISVKSFGEFEFWFAMIKIVTIILM 162

ILAILTASTERSNAI-DIKTLTEGLIAVAITVVAHLLGGRR----

----TL 91

VLLAYAICGIFİFFIMRAMGEMLYVEPSTGSFATFGHQYIHPMAGYITAMSNWFQWIIVG 102

ILLVVAVCAV-ITFALRAV-PFLILKPLRES-----

50 43

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; ORGANISM: Bacillus subtilis subsp. subtilis str. 168 US-60-556-841-11117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-60-556-841-11117; Sequence 11117, App.
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PRIOR APPLICATION NUMBER: US/09/721,495
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 60/159,015
PRIOR APPLICATION NUMBER: US 60/159,210
PRIOR APPLICATION NUMBER: US 60/159,210
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 60/172,979
PRIOR FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 25; Conserv
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                                                                                                                                    SEQ ID NO 11117
LENGTH: 462
                                                                                                                                                                                                                                                                        FILE REFERENCE: 38-21(53450)
CURRENT APPLICATION NUMBER: US/60/556,841
CURRENT FILING DATE: 2004-03-25
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PRIOR FILING DATE: 2000-10-10
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TITLE OF INVENTION: Chemokine Receptor
FILE REFERENCE: 019934-0007210US
CURRENT APPLICATION NUMBER: US/10/787,018
                                                                                                                                                                                                                  CURRENT FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 12463
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 LTASTFRSNAIDLKTLTF---GLIAVAITY 80
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Schall, Thomas J.
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TYPE: amino acid

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GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
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                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 5593:
                                                                                                                                                                                                                                                       FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 607012
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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LOCATION: (B) LOCATION 1...326
SEQUENCE DESCRIPTION: SEQ ID NO: 3665:
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ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 17-Apr-2003
PRIOR APPLICATION NUMBER: US/09/107,532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT
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ADDRESSEE: GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                       FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/417,884A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 100 Beaver Street
NAME/KEY: misc_feature
                                                                                                                      TOPOLOGY: linear
                                                                                                                                                               LENGTH: 117 amino acids
                                                                                                                                                                                                                         TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION DATA:
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                                                                                                                                            amino acid
                                        Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.8%; Score 72.5; DB 6;
27.4%; Pred. No. 0.64;
tive 16; Mismatches 38;
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
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RESULT 9 US-10-667-762-76

Sequence 76, Application US/10667762 GENERAL INFORMATION:

APPLICANT: Erding Hu

Yuan Zhu Ganesh M. Sathe Joyce Yue Mao

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RESULT 8
US-09-804-291A-449
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                                                                                                                                                                                                                                                                     ; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-291A-449
    昂
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/230,732
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/286,862
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 531
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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GENERAL INFORMATI
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                                                                                                                                                                                  Matches
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/804,291A
CURRENT FILING DATE: 2001-03-13
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/188,914
PRIOR APPLICATION NUMBER: 60/192,033
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/213,849
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/226,534
PRIOR FILING DATE: 2000-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/198,474
PRIOR FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/199,335
PRIOR FILLING DATE: 2000-04-24
PRIOR APPLICATION NUMBER: 60/207,702
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS FILE REFERENCE: 100337.54287US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                     Local
163 ----LIFSLPFRSHPIIPHFLCDILPVLRLASAGKHRSEISVMTATIVFI
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                                                                                          106 IVLGISECCLLTAMAYDRYVAICQPLRYSTLLSPRACLAMVGSSWLTGIITATTHAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 IDLKTLTF-GLIAVAITVVAHLLGGRRTLLSVGAGTIVFVGLVNL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 GHLPQINLENALASVPTLLAAILS--KSLLVIVLAGILSLSLIRL 116
                                             65 DLKTLTFGLIAVAITVVAHLL------GGRRTLLSVGAGTIVFV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 FSCILLVVAVÇAVITFALRAVPFLILKPLRESQFVGKMAMWMPAGIL-AILTASTFRSNA 63
                                                                                                                                                                             ch 13.5%;
l Similarity 26.4%;
29; Conservative 18
                                                                                                                                  8 ILLVVAVCAVITEALRAVPELILKPLRESQEVGK---MAMWMPAGILAILTASTERSNAI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                             ; Score 71; DB 5; Pred. No. 0.91; 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                          DB 5;
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                                                                                                                                                                               41; Indels
                                                                                                                                                                                                                             Length 313;
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18
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US-60-556-841-9476
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                                                                                                                                                                                                            ; ORGANISM: Oryza sativa
US-60-556-841-9476
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US-60-556-841-11808
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TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REPERENCE: 38-21(53450)
CURRENT APPLICATION NUMBER: US/60/556,841
CURRENT FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 12463
SEQ ID NO 11808
LENGTH: 568
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Best Local Similarity 31.3
Matches 36; Conservative
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CURRENT FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 12463
SEQ ID NO 9476
LENGTH: 618
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 9476, Application US/60556841
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 LVGLYVQSR-LYFGLGRDGLLPSVFAEVHPTRHTPVQSQIWVGCVAAVMAGLFNV 399
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                                                                                                                                    h 13.9%; Score 73; DB 7; Length 618; Similarity 29.1%; Pred. No. 1.2; 34; Conservative 17; Mismatches 44; Indels
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                                                       ACVILYVAVCIVIT----GMVPYTLIGEDAPLAEA-FAAKGIKFVTVLISIGAVAGLTTTL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACVLLYVAVCLVIT----GMVPYTLLGEDAPLAEA-FAAKGLKFITVLISIGAVAGLTTTL
                  TASTFRSNAIDLKTLTFGLIAVAITVVAHLLGGRRTLLS----VGAGTIVFVGLVNL 107
                                                                                              SCILLVVAVCAVITFALRAVPFLIL---KPLRESQFVGK------MAMWMPAGILAIL 54
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31.3%; Pred. No. 1.1;
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GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 11757
LENGTH: 618
TYPE: PRT
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Best Local Similarity
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TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERNCE: 38-21(53450)
CURRENT APPLICATION NUMBER: US/60/556,841
CURRENT FILING DATE: 2004-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 12463
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3665:
SEQUENCE CHARACTERISTICS:
                                                     PRIOR DATE: 17-Apr-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532

FILING DATE: 30-Jun-1998

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/551571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/417,884A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   377 LVGLYVQSRLYLGLGRDGLLP---SIFAKVHPTRHTPLHSQIWVGCVAAVLAGLFNV 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 TASTERSNAIDLKTLTFGLIAVAITVVAHLLGGRRTLLS----VGAGTIVFVGLVNL 107
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OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Waltham
STATE: Massachusetts
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29.1%;
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Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7;
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Result
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                       67.68
67.68
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seq length: 2000000000
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526
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| (cgn2_6/ptcdata/1/paa/US06_NEW_COMB.pep:*
| (cgn2_6/ptcdata/1/paa/US07_NEW_COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-724-972A-6988
US-60-556-841-11808
US-60-556-841-111808
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US-10-417-884A-5593
US-10-417-884A-5593
US-10-667-762-76
US-10-787-018-9
US-10-787-701-49503
US-60-556-841-1117
US-60-556-841-678
US-10-779-143433
US-60-556-841-678
US-10-756-841-678
US-10-756-841-11087
US-60-556-841-11087
US-60-556-841-11089
US-10-724-972A-4715
US-10-724-972A-4715
US-10-724-972A-4781
US-10-724-972A-4781
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US-60-556-841-1046482
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US-60-556-841-4550
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Sequence 698, Ap
Sequence 11808, A
Sequence 11808, A
Sequence 11857, A
Sequence 3655, Ap
Sequence 5593, Ap
Sequence 76, Appl
Sequence 76, Appl
Sequence 11117, A
Sequence 41503, Ap
Sequence 2298, Ap
Sequence 43433, A
Sequence 43433, A
Sequence 6678, Ap
Sequence 6678, Ap
Sequence 11087, A
Sequence 11087, A
Sequence 4153, Ap
Sequence 4715, Ap
Sequence 4715, Ap
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7889, Ap	6261, Ap	App	7473, Ap	6950, Ap	663,	5519, Ap	6530, Ap	*	4854, Ap	-	•	ъ,	3141, Ap	12239, A	4463, Ap	4458, Ap	5620, Ap	54323, A

ALIGNMENTS

Application US/10724972A

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; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 6988
; LENGTH: 156
; TYPE; PRT
; ORGANISM: S.epidermidis
US-10-724-972A-6988
                                                                                                                                                    US-60-556-841-8672; Sequence 8672, Application US/60556841; GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: DOUGETTE-Stamm, Lynn
APPLICANT: Bush, David
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/724,972A
CURRENT FILING DATE: 1903-12-01
PRIOR APPLICATION NUMBER: 09/450,969
PRIOR TILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 09/134,001
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21 (53450)
CURRENT APPLICATION NUMBER: US/60/556,841
CURRENT FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 12463
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US-09-328-352-6931
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US-09-489-039A-7704
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APPLICANT: GATY L. Breton et al.

APPLICANT: GATY L. Breton et al.

APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 6931

LENGTH: 169
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Matches
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PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5990
Sequence 7704, Application US/09489039A

Sequence 7704, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747
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Patent No. 6562958
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TYPE: PRT
ORGANISM: Proteus mirabilis
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20.4%; Pred. No. 0.35
ative 25; Mismatches
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; TYPE: PRT ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-7704
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Search completed: April 16, 2004, Job time: 11.2284 secs
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; NUMBER OF SEQ ID NO:
; SEQ ID NO 7704
; LENGTH: 188
                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Acinetobacter baumannii
US-09-328-352-6237
                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6237
LENGTH: 259
TYPE: PRT
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APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. BRETON et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
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Patent No. 6562958
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Similarity 22.4%; Pred. No. 0.69;
38; Conservative 24; Mismatches
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                                                                                                                                      KMLVLAGIGSLAIGFYDGIFGPGTGSFFIFFFIRFLQVDFLHASALSKIGNFMTNLAALS
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                                                                        FLIPTGHAILHIGLMMAAANVLGSIV-GVRTALKYGSGFVRIIFLILVSI
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19.8%; Pred. No.
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO A TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTI FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13014

LENGTH: 1049
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Best Local S
Matches 26
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GENERAL INFORMATION:
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                                            INFORMATION
                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: U11 2, 1997
                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: ATINIELLO, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                     MATION FOR SEQ ID NO: 559
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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ADDRESSEE: GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7310
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Similarity 19.4%; Pred. No. 2.2;
26; Conservative 23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Waltham
                                                                 TELEFAX:
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ENGTH:
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ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
ON: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
  117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 Beaver Street
                                                                 (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENOME THERAPEUTICS CORPORATION
                                              5593:
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27266
LENGTH: 303
TYPE: PRT
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Patent No. 6551795
GENERAL INFORMATION:
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                                                                                                               GENERAL INFORMATION:
                                                                                                                              Sequence 5990, Application US/09543681A Patent No. 6605709
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO
TITLE OF INVENTION: DIAGNOSTICS AND THERA:
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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LOCATION: (B) LOCATION 1...117
SEQUENCE DESCRIPTION: SEQ ID NO: 5593:
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                                                                                                                                                                                                                                                                                                                         90 MPAGLSSLVLQSQ---
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                                                                                                                                                                                                                                                                                                                                                                                                    35 DFPPLLF----CA-LRFALAALPLLVLRGPMPAPFGRILLIGVVLLGVVKFGLLFVGMAQG 89
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Pred. No.
                                                        AND AMINO ACID SEQUENCES RELATING AND THERAPEUTICS
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US-09-245-039-2
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                                  片
                                                                                                                                                                                                                                                                          ; TYPE: PRT ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-7412
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LENGTH: 1134
                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7412
LENGTH: 590
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Best Local (
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CURRENT APPLICATION NUMBER: US/09/245,039
CURRENT FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT: Chen, Yibang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Weinstein, Harel
APPLICANT: Buck, Elizabeth
TITLE OF INVENTION: PEPTIDES AND OTHER SMALL MOLECULES DERIVED FROM REGIONS
TITLE OF INVENTION: OF INTERACTING PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Iyengar, Srinivas R.V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT: Gary Breton et. al
ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
ITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS A
ILE REFERENCE: 2709.2004001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 AIGFGLVVAASHLLVTATLVPAKRPRLWRTLGANALLFLG-VNVY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 LALLESLTFALLCCPFALGGPAGAHAGAAAVPATADQGVWQLLLV-TFVSYALLEVRSLL 185
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                                                                        64
                                                                                                                  16 VVVCITALVIY----VPLLFIVVQSFLSAPFFSRSKSWSLEAFAFFFTDPDFYLALRSGF 71
                                                                                                                                                       10 LVVAVCAVITFALRAVP--FLILKPLRESQFVGKMAMWMPAGILAILTASTF----RSNA 63
                                                                                                                                                                                             1 Similarity
32; Conserv
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                                                                          IDLKTLTFGLIAVAIT----VVAHL-----LGGRRTL-----LSVGAGTIVFVG 103
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                                                                                                                                                                                               Conservative
                                    -LAFGLVIIAIFLGGILAFLMVRTDLÞGRRIIEÞLILVÞIFVSÞMVLGFGYVVAAG
                                                                                                                                                                                                              13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.3%; Score 75; DB 4; Length 1134; 28.6%; Pred. No. 1.2; tive 20; Mismatches 45; Indels
                                                                                                                                                                                           ; Score 73; DB 4; Length 590; pred. No. 0.94; 19; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUENCES RELATING TO KLEBSIELLA THERAPEUTICS
                                                                                                                                                                                                 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                        127
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                                                             US-09-489-039A-13014
                                                                              RESULT 9
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Sequence 13014, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:
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US-09-107-532A-3665

Sequence 3665, Applicati

Patent No. 6583275

PATENT INFORMATION:

APPLICANT: Lynn A
                                                                                                                                                                                                                     NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...
SEQUENCE DESCRIPTION: SEQ ID NO
US-09-107-532A-3665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  뮹
                                                                                                                                                        Matches
                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3665:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598
APPLICATION NUMBER: 60/085,598
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: pro
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 PVGFF 132
110 A----
                                    63 AIDLKTLTFGLIAVAITVVAHLLGGRRTLLSVGAGTIVFVGLVNLF 108
                                                                            ភូ០
                                                                                                                                                      29;
                                                                                                            8 ILLVV----AVCAVITFALRAVPFLILKPLRESQFVG-KMAMMMPAGILAILTASTFRSN 62
                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                         ILLVTRLPRTICLILVGATSSICGLIMQHLTQNKFVSPTTAGTMDSARLGILVAMIFLPG 109
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 326 amino acids
                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09107532A
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SE: GENOME THERAPEUTICS CORPORATION
  -SLIVRSLTAFCFAF--
                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                        13.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENTEROCOCCUS
                                                                                                                                                                                                                                                    SEQ ID NO:
                                                                                                                                                        16;
                                                                                                                                                                        Score 72.5; DB Pred. No. 0.52;
                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
    AGTLLFLSLTRLF 137
                                                                                                                                                        38;
                                                                                                                                                                                          Length 326;
                                                                                                                                                          Indels
                                                                                                                                                        23;
                                                                                                                                                        Gaps
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60/128,706

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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5172
ENOTH: 156
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US-09-134-001C-5172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5172
                                                                                                                                                                                                                                                       RESULT 4
US-09-540-236-2360
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Best Local (
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LENGTH: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5172, Application US/09134001C Patent No. 6380370
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                                                                                                                                                                                         Sequence 2360, Applic Patent No. 6673910 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/1
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
NUMBER OF SEQ ID NOS: 3840
EQ ID NO 2360
ENGTH: 506
                                                               CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
                                                                                                         APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2205-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 SKQGYILGLVQ-SISQFASMVG----IALGGGILVWFGLTTLF 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 IIAGCFIVTLLLAAV-----REISWFIGLYFLW---GILLGATTPVLTALISRSTAE 340
                                                                                                                                                                                                                                                                                                                                      103 DGVİQQHDHAFGYTLNLPYIİAIVPTVMLAIFTRSLTVTILGG---IFV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 VVAVCAVITEALRAVPELILKPLRE-SQFVGKMAMMPAGIL----AILTASTERSNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 DLKTLTFGLIAVAITVVAHLLGGRRTLLSVGAGTIVFVGLVNLF 108
                                                                                                                                                                                                                                                                                                                                                                              61
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Similarity 31.7%; Pred. No. 0.0012;
33; Conservative 18; Mismatches 30; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                              SNAIDLKTLTFG-----LIAVAITVVAHLLGGRRTLLSVGAGTIVFV 102
                                                                                                                                                                                                                                                                                                                                                                                                                        WITDLHTLVLIV-LCGVVTLLVRVIPFIMISRVNLPAIVIKWLSFIP---ITLFTÄLII-
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTTDFSCILLVVAVCAVITFALRAVPFLILKPLRESQFVGKMAMMMPAGILAILTASTFR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                     Application US/09540236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.7%; Score 82.5; DB 4; 25.7%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                Query Match
Best Local S
Matches 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47
                                                                        12 VAVCAVITEALRAVEELILKELRESOFVGKMAMMMPAGILAILTASTERSNAI----DLK 67
                                                                                                                    30;
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TYPE: PRT

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TLTFGLIAVA--ITVVAHLLGGRRTLL--SVGAGTIVFVGLVNLF 108

LALLFSLTFALLCCFFALGGFAGAHAGAAAVPATADQGVWQLLLV-TFVSYALLFVRSLL 185

45;

Indels

10;

Gaps

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; ORGANISM: M.catarrhalis
US-09-540-236-2360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-726-214-2
                                                                            US-08-726-214-2
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Patent No. 6107076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                      TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1134 amino acid
                                                                                                                                                                                                                                 FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tang, wearen APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN
TOTAL OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity tes 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewit
CLASSIFICATION: 435
                                                                                                 ropology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343 M 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 PAFETILIVVIVLSILMGNLLAIRQNNIKRM-LAYSSIAHIGYALTALLSIGAGSLPLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 VVMMLAAAAFKLSAAPFHSWVSDVYEGAPAPIAAFLASVSKVAMMALALRFFVGSMFTAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 VVAVCAVITFALRAVPF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houston
14.3%; Score 75; DB 3;
Similarity 28.6%; Pred. No. 1.2;
30; Conservative 20; Mismatches 4
                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAG---ILAILTASTFRSNAIDLKTLTFGLIAVAITVVAHLLGGRRTLLSVGAGTIVFVG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Arnold, Wh
                                                                                                                                                           1134 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                             Concurrently Herewith
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23.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   White & Durkee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of America
                                                                                                                                                                                                                                                                          UTSD: 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADENYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LILKPLRESQFVGKMAMWM 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #1.30
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                                         Length 1134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342
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Title:
Perfect score:
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No.
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.5
82.5
                              69.5
69.5
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70.5
70.5
70
70
70
70
70
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73.5
72.5
72.5
71.5
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| Compared_Patents_AA:*
| Compared_Patenta_2/iaa/5A_COMB.pep:*
| Compared_Patenta_2/iaa/5B_COMB.pep:*
| Compared_Patenta_2/iaa/6A_COMB.pep:*
| Compared_Patenta_2/iaa/6B_COMB.pep:*
| Compared_Patenta_2/iaa/PCTUS_COMB.pep:*
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US-09-245-039-7412
US-09-489-039A-7412
US-09-489-039A-13014
US-09-107-532A-5593
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Sequence 5, Appli
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	3478,	625, A	10320,	5620,	6747,	10, App	5981,	3286,	4387, Ap	,	•	9890, Ap	•	٠,	•	4353, Ap	Ī	`

ALIGNMENTS

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APPLICANT: SAHM, HERWANN
APPLICANT: SAHM, HERWANN
APPLICANT: SAHM, HERWANN
APPLICANT: BEGELING, LOTHAR
APPLICANT: PERFERLE, WALTER
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: SEANCHED CHAIN AMINO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/265496/MAS
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT APPLICATION NUMBER: DE 199-11-23
PRIOR APPLICATION NUMBER: DE 199-10-27
NUMBER OF SEO ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 108
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
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US-09-471-803A-5
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                                                                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: ATCC14752
US-09-471-803A-5
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                                                                                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 108; Conservative 0
    51
                             61 SNAIDLKTLTFGLIAVAITVVAHLLGGRRTLLSVGAGTIVFVGLVNLF 108
                                                                              \vdash
                                                                                                     1 MTTDFSCILLVVAVCAVITFALRAVPFLILKFLRESQFVGKMAMMMPAGILAILTASTFR
MTTDFSCILLVVAVCAVITFALRAVPFLILKPLRESQFVGKMAMMPAGILAILTASTFR
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                                                                                                                                                                              Score 526; DB 4;
Pred. No. 2.8e-58;
                                                                                                                                                             Mismatches
                                                                                                                                                                                                   Length 108;
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                                                                                                                                                             Gaps
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RESULT 2 US-09-543-681A-6109 Sequence 6109, Application US/09543681A
PATENT NO. 6605709
GENERAL INFORMATION:
APPLICANT: GARY ERETON
TITLE OF INVENTION: DUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII
TITLE OF INVENTION: DUGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A

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Search completed: April 16, 2004, 06:53:15 Job time: 34.3844 secs
                                                                                                                                                                                                                                                                                                                     Query Match 14.5%; Score 76.5; DB 4; Length 440; Best Local Similarity 26.1%; Pred. No. 1.1; Matches 35; Conservative 19; Mismatches 35; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium. And identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-DEC-1999; 99JP-00377484.
07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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N-PSDB; AAH67841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakagawa S,
Tateishi N,
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; SEQ ID NO 6376; 246pp + Sequence Listing; English.
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                                                                                 317 DDRVGPKPİILISL 330
                                                                                                                                                                262
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                                                                                                                                                              FLIAAAVFRDGLAGVETFGAILAVSVYGLSAGDV--LLFGVAANVVSALGALLGG---FL 316
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Senoh A, Ikeda M, Ozaki A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cc pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an corganism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene cc compound's activity; (11) a culture comprising strains in which the gene cc product is overexpressed or underexpressed; (12) determining the extent ct to which each of the strains is present in a culture or collection of creations; or (13) identifying the target of a compound that inhibits the creation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational cfor cellular proliferation to isolate candidate molecules for rational cforguired for proliferation in cells other than S. aureus, S. typhimurium, crequired for proliferation in cells other than S. aureus, S. typhimurium, crequired for prokaryotic essential genes. Note: The sequence data for this content did not form part of the printed specification, but was obtained content of the print of specification, but was obtained content of the print of specification of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of t
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Best Local S
Matches 30
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01-JUL-1999;
01-JUL-1999;
08-JUL-1999;
08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum; stress; resistance; tolerance; SRT; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; evolutionary study; environmental hazard; fermentation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C. glutamicum SRT protein sequence SEQ ID NO:268.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 LÍTFLÍSLFAFIÍLEKHSKNPMINLNLFKIREFTASALVALLAQFFYIGVIVIL--PTFF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SNAIDLKTLTFGLIAVAITVVAHLLGGRRTLL--SVGAGTIVFVGL 104
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99DE-01031541.
99DE-01032200.
99DE-01032230.
99DE-01032231.
                                                                                                      99DE-01040764.
99US-0151214P.
                                                                                                                                                                                                                                                                                             99DE-01030429.
99US-0142692P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glutamicum.
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28.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Mismatches
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0.99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
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Sequence 440 AA;

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cc expression in host cells and production of fine chemicals, such as, an cc arganic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a cc saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine cc chemical production can be modulated. The presence of (I) or the SRT cc proteins (III) encoded by them are used for diagnosing the presence or activity of Corynebacterium diphtheriae. (I), (II), (III) and host cells containing them can be used to map the genomes of organisms related to C. glutamicum, to identify and localise c. glutamicum sequences of interest, in evolutionary studies, in determination of SRT protein regions required for function, in modulating the SRT protein activity, and in modulating the sRT protein activity, and in modulating the sRT protein activity, and in modulating the sRT protein activity, and in modulating the sRT protein activity, and in modulating the sRT protein activity and in modulating the sRT protein molecules encoded by it increase the survival of C. glutamicum to chemical and environmentally or chemically conditions. By increasing the growth rate or maintaining a normal growth rate in poor or toxic conditions, the yield, cc culture may he increased
AAF70984 to AAF71133 encode the Corynebacterium glutamicum stress, resistance, and tolerance (SRT) porteins given in AAB78871 to AAB7 The C. gluttamicum SRT genes (I) can be used in vectors (II) for expression in host cells and production of fine chemicals, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Corynebacterium glutamicum nucleic acid encoding a tolerance or resistance protein, for production or modulation of production of fine chemicals, such as, e.g. amino acids, lipids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pompejus M, F
Lee H, Kim H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 481-482; 526pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carbohydrates,
                                                culture
                                             may
                                             be increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kroeger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or enzymes.
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밁 S 밁 밁 Ś Ś Best Local Matches Query Match 317 262 FLIAATVFRDGLAGVFTFGAILAVSVYGLSAGDV--LLFGVAANVVSALGALLGG---FL 202 LVAVLAAVWĖLVSAIPALLRVĖEIĖAQVAAEDHPKGLIAAYKDLEGQIAELWKQDRNSVY 93 S--VGAGTIVFVGL 48 -----AGIL---AILTASTFRSNAIDLKTLTFGLIAVAITVVAHLLGGRRTLL 11 VVAVCAVITFALRAVPFLILKPLRESQ------FVGKMA-MWMP----l Similarity 35; Conserv DDRVGPKPIILISL 330 Conservative 14.5%; 104 19; Score 76.5; Pred. No. 1. Mismatches DB 4 35; Length 440; Indels 45; Gaps 92 261 47

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RESULT 15
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                                                                                           C glutamicum protein fragment
                                                                                                                                                                            AAG92622 standard; protein; 440
                           Corynebacterium
                                                    Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
                                                                                                                       26-SEP-2001
                                                                                                                                                   AAG92622;
                                                                                                                       (first entry)
                                                                                              SEQ ID NO: 6376.
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(BADI) BASF

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Similarity

DB 4;

Length 314;

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RESULT 12
ABM67632
ABM67632
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Best Local S
Matches 20
                            response or sensitivity to toxins and antibiotics produced by P. luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-encoded toxins or antibictics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                        proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2001; 2001FR-00001659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-2002; 2002WO-IB003040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM67632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200294867-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duchaud E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Photorhabdus luminescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 whooping cough
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06-SEP-2001; 2001US-00948993;

25-OCT-2001; 2001US-0342923P

08-PEB-2002; 2002US-00072851

06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Wall D,
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Trawick JD,
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Forsyth
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological

Claim 25; SEQ ID NO 72462; 1766pp; English.

Claim 6;

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665; 192pp; French

Gaps

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Staphylococcus epidermidis; open reading frame; \mathtt{ORF}_i bacterial infection; antibacterial; gene therapy.
          Claim 1; SEQ ID NO 5172; 267pp; English
                             Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infec
                                                        WPI; 2002-381255/41.
N-PSDB; ABN92872.
                                                                                                                                     14-AUG-1997;
                                                                                                                                                                           30-APR-2002
                                                                                                                                                                                             US6380370-B1
                                                                                                                                                                                                                 Staphylococcus
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                                                                                                                           97US-0055779P.
97US-0064964P.
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                                                                                                          THERAPEUTICS CORP
                                                                                                                                                         98US-00134001
                                                                                                                                                                                                                                                                                                                        protein; 156
                                                                                       Bush
                                                                                                                                                                                                                                                                 amino acid sequence SEQ ID NO:5172
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Sequence

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AAH75903-AAH75920

and AAG66436

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The present invention relates to the genome sequence of Listeria componery cogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes—related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. concortogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained or form intentional or treatment or prevention of infections by L. content of the printed specification, but was obtained or form intentional or treatment or prevention of infections by L. content of the printed specification, but was obtained or form intentional or treatment or prevention of infections and cell intention of the printed specification at the sequence of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 156 AA;
                                                                                                        The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAP66431 and AAH41223-7) and P. abyssi proteins. P. abyssi abyssi (see AAP66431 and AAH41223-7) and P. abyssi proteins. P. abyssi proteins a hyperthermophilic archaeon, which is isolated from deep-sea hydrochermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up in 10 degrees centigrade. Note: This patent is in the same patent family (MC20065062, which contains additional sequences as shown in AAB99132-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Forterre P,
Querellou J,
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Pred. No. 0
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RESULT 10 ABP40327

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62 99 Query Match Best Local S Matches 29

Similarity

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Sequence 108 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cc preferably ADGUC sequences are useful in the diagnosis, prevention and cc polypeptides. ADGUC sequences are useful in the diagnosis, prevention and ct treatment of cardiovascular disorders (e.g. angina pectoris, myocardial cc infarction, ischaemic heart disease, hypertension and atherosclerosis), cc vision disorders (e.g. keratoconjuctivitis sicca, keratitis, iritis, cc etaract), neurological disorders (e.g. epilepsy, Alzheimer s disease, cc pick's disease, Huntington's disease, demantia, Parkinson's disease, cc reproductive disorders (e.g. infertiality, Parkinson's disease, cc reproductive disorders (e.g. infertiality, endometricis, impotence, cc uterine fibroid and gymaecomastia), smooth muscle disorders (e.g. cranhythmias, asthma and migraine) and bacterial infections. ADGUC collymucleotides are useful for creating knock-in humannised animals or transgenic animals to model human diseases. They are useful in somatic or germline gene therapy. ADGUC polymucleotides are also useful for collymucleotides are useful in a number of drug screening techniques and in cc vaccines. The present sequence is human ADGUC-5 protein
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                                                                                                                                                                                                                                                                                                        antiparkinsonian; cerebroprotective; analgesic; ant antiinflammatory; gene therapy.
                                                                                                                      29-OCT-2001; 2001US-0330710P.
23-JAN-2002; 2002US-03500139.
19-JUN-2002; 2002US-0389538P.
26-SEP-2002; 2002US-0413597P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1119 AA;
                WPI; 2003-441359/41.
N-PSDB; ACC58111.
                                                                                                                                                                                                   29-OCT-2002; 2002WO-EP012059.
                                                                                                                                                                                                                                                              WO2003038083-A1.
                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    Human type I adenylate cyclase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; protein; 1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 131-133; 167pp; English.
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                                                                                                                                                                                                                   Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Medjari H, Glaser P, Kunst F, Cossart Daniels J, Goabel W, Kreft J, Kuhn M, Ne F, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listeria monocytogenes protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAVCAVITEALRAVPELILKPLRESQFVGKMAMMMPAGILAILTASTERSNAI----DLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.2%; Scc
31.4%; Pro
1tive 18;
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Pred. No. 0.29
18; Mismatches
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Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections, polypeptides.

for treatment

and related

WPI; 2002-010914/01.

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RESULT 6
ABR42400
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Matches
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            The present sequence is the protein sequence of a splice variant of human type I adenylate cyclase (see also ARR42399), an enzyme that catalyses the synthesis of cAMP from ATP. The invention provides reagents that regulate human type I adenylate cyclase gene products. These reagents which bind human type I adenylate cyclase snooding e.g. present sequence, can be used to modulate the activity of human type I adenylate cyclase in a disease, especially a central nervous system (CNS) disorder, diabetes and chronic obstructive pulmonary disorder (claimed). The CNS disorders may include Alzheimer's disease, Parkinson's disease, stroke or neuropathic pain.

Type I adenylate cyclase can be obtained by recombinant methods, and used to screen for activator and inhibitor compounds
                                                                                                                                                                                                                                                                                                                                                            29-OCT-2001; 2001US-0330710P
27-002 2002US-0350019
26-SEP-2002; 2002US-0389538P
26-SEP-2002; 2002US-0413597P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiparkinsonian;
antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adenylate cyclase; enzyme; human; neuroprotective; nootropic; antiparkinsonian; cerebroprotective; analgesic; antidiabetic;
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                                                                                                                                                                                                              New polynucleotide encoding a type I adenylate cyclase polypeptide, useful for diagnosing, preventing or treating diseases associated with type I adenylate cyclase dysfunction, e.g. CNS disease or diabetes.
                                                                                                                                                                                                                                                                 WPI; 2003-441359/41.
N-PSDB; ACC58112.
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                                                                                                                                                                                      Claim 1; Page 139-140; 167pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STFRSN-----AIDLKTLTFGLIAVAIT-VVAH--LLGGRRTLLSVGAGTIVF-VGLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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Pred. No. 0.029;
21; Mismatches 39;
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RESULT 7
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                                                                                                                               31-AUG-2000;
22-SEP-2000;
29-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                             Human; adenylyl and guanylyl cyclase; ADGUC-5; cardiovascular disorder; angina pectoris; myocardial infarction; vision disorder; keratitis; cataract; neurological disorder; epileps; Alzheimer's disease; pick's disease; troke; mental disorder; mood and anxiety disorder; reproductive disorder; infertility; endometriosis; impotence; asthma; smooth muscle disorder; migraine; bacterial infection; gene therapy;
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                                                                            Gandhi
Baughn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-2002
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                                                                                                                                                            29-JUN-2000;
04-AUG-2000;
                                                                                                                                                                                                                                                                  Domain
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                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic animal; vaccine; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human adenylyl and
      Novel human adenylyl and guanylyl cyclases and polynucleotides encoding the cyclases, useful for treating, diagnosing or preventing cardiovascular, neurological, vision, reproduction and smooth muscle
                                                   N-PSDB;
                                                                                                                                                                                           26-JUN-2001; 2001WO-US020491
                                                                                                                                                                                                                10-JAN-2002.
                                                                                                                                                                                                                                   WO200202757-A2
                                                                                                                                                                                                                                                                                     Domain
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                                                                                                           (INCY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                           2002-154740/20.
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                                                  AAD28061.
                                                                                                           INCYTE GENOMICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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                                                                                                                               ; 2000US-0215476P.
; 2000US-0223545P.
; 2000US-0229876P.
; 2000US-0234838P.
; 2000US-0236483P.
                                                                              Tribouley
Thornton M
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                                                                                                                                                                                                                                                                  987.
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294. .478
                                                                                                                                                                                                                                                                                                                   note=
                                                                                                                                                                                                                                                                                                                                     note= "Guanylate cyclase motif"
                                                                                                                                                                                                                                                                                                                                                          note= "Adenylate and guanylate cyclase catalytic
                                                                                                                                                                                                                                                        note=
                                                                                                                                                                                                                                                                           'note= "Adenylate
                                                                                                                                                                                                                                                                                              notes
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                                                                              Ding L,
Yao MG,
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Pred.
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                                                                               Lu DAM,
Walia NK,
                                                                                                                                                                                                                                                       cyclase motif"
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                                                                                                                                                                                                                                                                                                domain"
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                                                                               Tang
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Best Local Similarity
                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                    The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55221). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent w0200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at the production of format directly from WIPO at standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleotide sequence useful in the identification or Lactococcus lactis and related species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-043418/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus lactis; IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactococcus lactis protein yqfC
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                                                                                                                                                                                                                                                                                                                                                     Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6;
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                                                     62 NAIDLKTLTF-GLIAVAITVVAHLLGGRRTLLSVGAGTIVFVGLVNL 107
                                                                                                                                                                                                                                    32;
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                                                                                                                                                                            3 TDFSCILLVVAVCAVITFALRAVPFLILKPLRESQFVGKMAMMMPAGILAILTAST-FRS 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1660; 2504pp; French.
                                                                                                                   SSFEF1SLT11GCAIVTWISRVLPFILLKKMSLPQIVVEYLSFVPVVIMSALWISNLF1Q
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29.9%; Pred. No. 0.00
tive 24; Mismatches
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16; Mismatches 47
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                                                                                                                                                                                                                                                                                         Length 108;
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ct the 6213 antisense sequences given in the specification where expression confirmed the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid conding a polypeptide whose expression is inhibited by the antisense concluded acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense concluded; (2) a nantibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway for a gene product or that has an activity against a biological pathway or againsm acts; (9) manufacturing an antibotic; (10) profiling a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; activity; (11) a culture comprising strains in which each of the strains is present in a culture or collideration of an organism configuration to isolate candidate molecules for rational configuration of an organism. The antisense; (12) determining the extent to which each of the strains is present in a culture or collection of configuration of an organism. The antisense nucleic acids are useful for cellular proliferation of acids or homologous nucleic acids required for proliferation to isolate candidate molecules for rational configurated for proliferation in cells other than S. aureus, S. typhimurium, C. patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at figure data for this configuration, but was obtained configuration. The present sequence data for this configuration, but was obtained configuration. The present sequence are obtained configuration. The present sequence are obtained to the trained proliferation of the printed specification, but was obtained configuration. The present sequen
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIT-)
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Trawick
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Carr GJ,
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Forsyth
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 108
The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, calcided to the particularly L-lysine. The present sequence is a protein described in the
                                                                                                                                                                                                                                                                                                                 Nakagawa
Tateishi
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07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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                                                                                                                                                                                               Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
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                                                                                                                                                                   Claim 17;
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DB; AAH65255.
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Senoh A,
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Ikeda M,
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Matches 108
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07-APR-2000;
03-AUG-2000;
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                                            The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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Tateishi
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DB; AAH68372.
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Senoh A, Ikeda M,
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Pred. No. 4.1e-57;
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Ozaki A;
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Post-processing: Minimum Match 0%
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1: geneseqD1980s:*
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Gapop 10.0 , Gapext 0.5
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1004.303 Million cell updates/sec
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Aag93036 C glutami
Aab93153 C glutami
Abb54958 Lactococc
Abu45714 Protein e
Abr42400 Human typ
Aae17133 Human ade
Abr42399 Human typ
Abb47960 Listeria
Abp40327 Staphyloc
Aab96384 Putative
Abm67632 Photorhab
Abu44538 Protein e
Aab79004 C. glutami
Aag92622 C glutami
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S. Cinnam
N. gonorr
Human olf
Human G p
Human olf
Human G-p
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Adenylyl
Bovine ad
Sequence
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4. U	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
71.5	72	72	72	72	72	72.5	72.5	72.5	73	73.5	73.5	73.5	73.5	73.5	74	74	74	74	74
13.6	13.7	13.7	13.7	13.7	13.7	13.8	13.8	13.8	13.9	14.0	14.0	14.0	14.0	14.0	14.1	14.1	14.1	14.1	14.1
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AAU38126	ABR42401	ABU21547	ABR42402	ABB67164	ADC95966	ABU28297	ABU32055	ADC94038	ABM72816	ABU15219	AAU34479	AAY32855	ABU24119	ADB12425	ADC86129	AAG72225	AAG72535	ABR01631	ADC85887
Aau38126 Salmonell		_			σ	Protein		4038	2816 Sta	Protein	479 E. coli	Aay32855 E. coli a	119 Pro	Adb12425 Alloiococ	9	Human ol	5 Human OR	Human	Adc85887 Human GPC

ALIGNMENTS

RESULT 1 AAB86248 ID AAB8 C. glutamicum brnE protein 05-SEP-2001 AAB86248; AAB86248 standard; protein; 108 WPI; 2001-391595/42. N-PSDB; AAH21109, AAH21111. 27-OCT-1999; Corynebacterium glutamicum L-amino acid production; brnF; brnE; branched-chain amino acid; coryneform bacterium; leucine; isoleucine; valine; medicine; New export genes from coryneform bacteria, useful for increasing fermentative production of branched-chain amino acids. Kennerknecht N, 11-OCT-2000; 2000EP-00122057. EP1096010-A1. animal nutrition. (DEGS) 02-MAY-2001. DEGUSSA AG. FORSCHUNGSZENTRUM JUELICH GMBH. (first 99DE-01051708 Eggeling L, entry) Sahm H, ጅ Pfefferle W;

This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) polypeptides; (ii) encodes a polypeptide at least 70% identical with (3) or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least 15 consecutive bases from (i)-(iii). The invention also describes (a) protein derived from sequences of 753 bp (2) or 324 bp (4); (b) coryneform microorganisms, especially Corynebacterium, transformed with one or more (I), where these are replicative DNA; (c) production of branched-chain L-aa by fermentation of coryneform bacteria in which the brnE and/or brnF genes (or equivalent sequences) are amplified,

least

Claim la; Page 17; 23pp; German.

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AUTHORS
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CK295424
LOCUS
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JOURNAL
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                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                          Matches 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicotiana benthamiana

Nicotiana benthamiana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Solanales; Solanaceae; Nicotiana.

E 1 (bases 1 to 936)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,

Staskawicz, B., Jin, H. and Baker, B.

Generation of EST sequences from Nicotiana benthamiana

Unpublished (2003)

Other ESTs: EST758139

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTGGTGGCGCATCTTC 253
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                                               GGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTTCGCAGGAATGCGATAG
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     GGATGATACCACAAGTGTTTTCATTTGCTTTGGAATTCCCCAATTATGAAGTTTTTGCAAG
                                                                                                  TTCTAATGTTAATCGGTCAGCCCGAAAACATCTCAAGGTGGGCGGGGAAATTCGCGCTGT 478
                                                                                                                                                                                     10.7%;
ilarity 47.5%;
Conservative
                                                                                                                                                                                                                                                                                                    /lab host="DHIOB-TonA"

/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pONVSport6.1, Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (5 E c 3 hr, 6hr), and pathogen
challenged leaves (5 E c 3 hr, 6hr), and pathogen
campestris pv campestris 12 hr, 18hr;
Resudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="abiotic and biotic stress-treated leaves, callus tissue_and_root_tissue"
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|mol_type="mRNA"
|db_xref="taxon:4100"
|clone="NBMCU77"
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                                                                                                                                                                                                              Score 34.6;
Pred. No. 26;
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                                                                                                                                                                                                                                     Length 936;
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Search completed: April 17, 2004, 20:01:47 Job time : 1053.18 secs

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RESULT 13
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Buell, C.R., Hart, A., Zigmann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana Unpublished (2003)
Contact: Robin Buell
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Clones can be requested from TIGR via potato@tigr.org
Seg primer: ATT TAG GTG ACA CTA TAG.
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1 (bases 1 to 922)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
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Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
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The Institute for Genomic Research
9712 Medical Center Dr, Rockville,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGG 290
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/tissue type-whitch and biotic stress-treated leaves, callus tissue and root tissue"

/lab host="DH10B-TonA"

/lab host="DH10B-TonA"

/clone lib="Nicotiana benthamiana mixed tissue cDNA

library, normalized, full-length"

/note="Vector: pcMVSport6.1; Site_1: EcoRI; Site_2: NotI;

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/note="vector: pcMVSport6.1; NotI;

/note="vector: pcMVSport6.1; NotI;

/note="vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Nicotiana benthamiana'
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4100"
/clone="NBMCX72"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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GGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTTCGCAGCAATGCGATAG TTCTAATGTTAATCGGTCAGCCCGAAAACATCTCAAGGTGGGCGGGGAAATTCGCGCTGT TTCCGTTCTTAATCCTTAAGCCCCCTACGTGAATCACAATTTGTGGGCAAAATGGCGATGT

Conservative

0

Score 34.6; DB 14; Pred. No. 26; 0; Mismatches 114;

Indels Length

0

agas

554 193

133 0 922;

10.7%;

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB239541 two-month-old roots from clone 'Beaupre' grown for 19 days under restricted irrigation Populus balsamifera subsp. trichocarpa x Populus deltoides cDNA 5', mRNA sequence.
CB239541 CB239541.1 GI:30233030
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Equipe de Microbiologie Forestiere
Institut National de la Recherche Agronomique
Centre INRA de Nancy, 54280 Champenoux, Francy
Tel: +33 383 39 40 80
Fax: +33 383 39 40 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: fmartin@nancy.inra.fr
Insert Length: 413 Std Error: 0.00
Seq primer: Fornat 5', AAGCGCGCCATTGTGTTGGTACCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Populus balsamifera subsp. trichocarpa x Populus deltoides Populus balsamifera subsp. trichocarpa x Populus deltoides Populus balsamifera subsp. trichocarpa x Populus deltoides Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kohler,A., Delaruelle,C., Martin,D. and Martin,F. The poplar root transcriptome: analysis of 7000 e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTCTCATTGCCGTTGCGATTACAGTGGTGGCGCATCTTCTTGGCGGTCGACGCACCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uds; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus. (bases 1 to 413)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo (dT)
/note="Ist strand cDNA was primed, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martin FM
                         /dev_stage="two-month-old"
/clone lib="two-month-old roots from clone 'Beaupre' grown for 19 days under restricted irrigation"
/note="Organ: root; Vector: pTriplEx2; cDNA library of roots from two-month-old Populus trichocarpa Torr.& Gray x deltoides Bartr. Ex Marshall (clone 'Beaupre') grown for 19 days under restricted irrigation to reach 50% of the transpiration rate of fully watered plants. The cDNA library was constructed from 1 ug of total RNA using the SMART cDNA synthesis kit (clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. The
                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Populus balsamifera subsp. trichocarpa
Populus deltoides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       db_xref="taxon:3695"
                                                                                                                                                                                                                                                                                                                                                    cultivar="'Beaupre'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%;
                                                                                                                                                                                                                                                                                                                                                                           type="mRNA"
cDNA was packed into
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Pred. No. 25
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                            Query Match 10.7%;
Best Local Similarity 47.5%;
Matches 103; Conservative
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ACCESSION VERSION KEYWORDS

ORGANISM

JOURNAL COMMENT

FEATURES

0

Score 34.6; D Pred. No. 25; O; Mismatches

DB 14;

Length Indels

853;

° ,,

Gaps

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REFERENCE AUTHORS

TITLE

RESULT 11 CB239541

DEFINITION

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Matches

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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asteriob; Lamino, Common asteriob; Lamino, L., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker B. Staskawicz, B., Jin, H. and Baker B. Generation of EST sequences from Nicotiana benthamiana Unpublished (2003)
Other ESTs: EST766192
Contact: Robin Buell
The Institute for Genomic Research
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131
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EST760191 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NBMD912 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Nicotiana.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 60.
55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGGTTCCGGCGGCCACCAGGNTTCCTGGC 161
/tissue type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"

/lab host="DH10B-TonA"

/clone_lib="Micotiana benthamiana mixed tissue cDNA
library_normalized, full-length"

/note="Vector: pcW/Sport6.1; Site_1: EcoRI; Site_2: NotI;
supplier: RNA was isolated from Micotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Nicotiana/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="NBMD912"
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Pred. No. 19;
0; Mismatches
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format
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                                                                                                                                                                                                                                                                                                                                                                                                                                       808 bp mRNA linear EST 05-JUL-2001
602907255F1 NCI CGAP_Kid14 Mus musculus cDNA clone IMAGE:5064373
5', mRNA sequence.
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Wellcome Trust (Dentre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing pipeline with 384 multicapillary sequencer.
10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                 BI144284
BI144284.1 GI:14604285
EST.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contail: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green,
cDNA Library Preparation: Life Techno
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 808)
                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                                              musculus (house mouse)
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/tissue_type="activated spleen"
/clone_lib="RIKEN full-length enriched, activated
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/mol_type="mRNA"
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Pred. No. 20;
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High quality sequence stop: 793.
Location/Qualifiers
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11173 row: m column: 14
                                                                                                         Email: Seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4682.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
ogi-bin/cluster.cgi?seq=CS0A1052DA090Pl&cluster=4682.r. Contact
Peng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0AI052DA09QPl.
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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BP 191 91006 EVRY cedex - France
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/clone="IMAGE:5064373"
/clone=lib_most=mbH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Site_2: SalI; Cloned unidirectionally. Primer: Oli Site_2: SalI; Cloned unidirectionally. Primer: Oli Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. |"
                                                                                        Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                           Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and haaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Cancer instituted by Dartial Bogenic strain y2; cn bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 1101)
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AL056828.1 GI:4937496
GSS.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOFO; Site_1:
/note="Vectod genomic DNA library"
                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                      /clone="BACR23H11"
/clone_lib="RPCI-98"
/note="end : TET3"
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Pred. No. 18;
81; Mismatches
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Pred. No. 1
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                                                                                Nikaido, I., Osato, N., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Schonbach, C., Gojobori, T., Schriml, L.M., Kanapin, A., Matsuda, H., Batlov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Eletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Chothia, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Nallais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Mallais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Nallais, L., Paran, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Schow, M., Shimada, K., Sultana, R., Schneider, C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wallestedt, C., Wang, Y., Watanabe, Y., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Yang, L., Yuan, Z., Zavolan, M., Shiwad, R., Vang, S., Watanabe, Y., Yang, L., Walle, R.D., Tomita, M., Yang, I., Yang, L., Walle, R.D., Shiraki, T., Waki, K., Kawai, J., Jazwa, K., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Janawa, K., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Jander, E.S., Rojers, J., Birney, E. and Hayashizaki, Y., Sakaski, D., Shibata, K., Sakaski, D., Shibata, K., Sakasi, K., Sakaski, D., Shibata, K., Sakasi, K., Sakasi, K., Sakasi, K., Sakasi, K., Sakasi, K., Sakasi
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Mus musculus
Mus musculus
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BY765711 GI:27203910
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1, activated spleen
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en Mus musculus
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group,
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (1
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagaw

Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(RIKEN) RIKEN

Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Adachi,J., Aizawa,K., Akimura,T.,

Arakawa, T., Carninci, P.

Fax: 81-45-503-9216

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KEYWORDS
SOURCE
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VERSION
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BZ720836
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JMT--08-M05.bl AtJMT-overexpressing transgenic rice
libzary (JMT) Oryza sativa cDNA clone JMT--08-M05, m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeenggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 475)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., L.
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                                                                                                                                            genomic survey sequence
BZ720836
BZ720836.1 GI:28512409
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               Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 786)
Whitelaw, C.A.,
                                                                                        Zea mays
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                                                                                                                                                                                                                                                                                                                 CACGGCCTTCAGAGAAGCCATTCTTCTGATGCTTCTCTGCTCTGTTCT 88
                                                                                                                                                                                                                                                                                                                                                 AACGTTTCGCAGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCT 218
                                                                                                                                                                                                                                                                                                                                                                                        CGGGCTTGTCGCCGTCTCACTGAGCTTGGCAGCCGGCTCCTTGGCAAGTCCGGCAGGTTT
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="JMT--08-M05"
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/lab_nost=="E.coli DH10B"
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/note="Vector: pCR4-TOPO; Site_1: EccRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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 Quackenbush, J.,
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; Pred. No. 13;
0; Mismatches
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3 Zea mays
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 Van Aken,S.,
                                                                                                                                                                                                   DNA linear GSS 24-FEB-2003 genomic clone ZMMBTa137A09,
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   Utterback, T.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                              1 (bases 1 to 910)
Whitelaw, C.A., Quackenbush, J., Var
Resnick, A., Fraser, C.M., Yuan, Y.,
                                                                            Seq primer: TF
Class: sheared ends
                                                                                                                            9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                      Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUHTK88TB
                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mayв
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                                                                                                              Email: whitelaw@tigr.org
                                                                                                                                                                                                       Contact: Cathy Whitelaw
/organism="Zea mays"
/mol_type="genomic DNA"
                                                       Location/Qualifiers
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Rockville,

MD 20850, USA

Van Aken,S., Utterback,T., Y., San Miguel,P., Ma,J. and

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249 TCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTTTTTGTTGG
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Maize Genomics Consortium
Unpublished (2003)
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Fax: 301-838-0208
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CC362201.1 GI:30831601
                                                                                      puntx88TD ZM_0.6_1.0_KB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Resnick, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                    TATGTTGCACATGTGC 615
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Pred. No. 16;
0; Mismatches
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                                                                                                                                 910 bp DNA linear GSS 16-MAY-2003
Zea mays genomic clone ZMMBTa530007,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pacs1-60 663.sl pacs1-60 Pseudomonas pacs1-60_663, genomic survey sequence BZ557685
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                 University of Washington
Box 352145, Seattle, WA 98105-2145,
                                                                                                                                                                                                                                                                                                                         Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                         Burns, J.L., Kaul, R. and Olsen, M.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa
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                                                                                                                                                                                                       Class: shotgun.
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                                                                                                                                                                                                                                                                                                                                               Contact: Chris K.
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1 (bases 1 to 1353)
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                                                                                                                                                                                                                          craymond@u.washington.edu
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/mol_type="genomic_DNA"
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                                                                                          db_xref="taxon:287"
                                                                                                                                              organism="Pseudomonas
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Lazge-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                       85
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Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                   AACGTTTCGCAGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCT 218
                                                                                                         ATTTGTGGGCAAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATC 170
CACGGCCTTCAGAGAAGCCATTCTTCTGATGCTTCTCTGCTCTGTTCT
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/clone="7LEAF--08-E15"
/tissue_type="leaf"
/tissue="ype="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was cappe
with oligoribonucleotides and then used as templates fc
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/mol_type="mRNA"
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                                                                              Pred. No. is the number of results prescore greater than or equal to the scand is derived by analysis of the total
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COMMENT	RESULT 1 CNSO05NG/ LOCUS DEFINITIO ACCESSION VERSION KEYWORDS SOURCE ORGANIS REFERENCE AUTHORS TITLE JOURNALL	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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P 191 91006 EVRY Cedex - FRA Web: www.genoscope.cns.fr) Web: www.genoscope.cns.fr) Web: www.genoscope.cns.fr) Determination of this BAC-end ollaboration with the Berkel he BDGP is constructing a ph elanogaster genome using the lease see http://www.fruitf elanogaster BAC library was aron Mammoser in Pieter de J	CNS005NG CNS005NG Drosephila melanogaster genome BACR12G04 of RPCI-98 library f fly), genomic survey sequence. AL060428 AL060428.1 GI:4943359 GSS. Drosephila melanogaster Eukaryota; Metazoa; Arthropoda Meoptera; Endopterygota; Dipte Ephydroidea; Drosephilidae; Dr 1 (bases 1 to 995) Direct Submission Direct Submission Direct Submission Submitted (02-JUN-1999) Genosc	
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BP 191 91006 EVRY cedex - FRANCE (E-mail: BP 191 91006 EVRY cedex - FRANCE (E-mail: B - Web: www.genoscope.cns.fr) Determination of this BAC-end sequence was collaboration with the Berkeley Drosophila G The BDGP is constructing a physical map of the melanogaster genome using these BACs. For fu please see http://www.fruitfly.org The BDGP melanogaster BAC library was prepared by Kaz Aaron Mammoser in Pieter de Jong's laborator	CNS005NG 995 bp DNA 1 Drosophila melanogaster genome survey sequence BACRI2G04 of RPCI-98 library from Drosophila fly), genomic survey sequence. AL060428 AL060428.1 GI:4943359 GSS. Drosophila melanogaster (fruit fly) Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Ir Eukaryota; Endopterygota; Diptera; Brachycera Ephydroidea; Drosophila. 1 (bases 1 to 995) Genoscope. 2 United Submission Submitted (02-UN-1999) Genoscope - Centre N	AW456947 AW457742 AW487742 AW489067 BEF460793 BI114807 BI114847 BI114847 BI1911653 BI9011653 BI9011912 BF207637 AK083916
Cache	CNS005NG CNS005NG CNS005NG Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR12G04 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence. AL060428 AL060428.1 GI:4943359 GSS. Drosophila melanogaster (fruit fly) Drosophila melanogaster (fruit fly) Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 995) Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:	AW456947 UI-M-BH3- AW491785 UI-M-BH3- AW491785 UI-M-BH3- AW49067 UI-M-BH3- BF460793 UI-M-CB9- BI134847 UI-M-BH3- BI901653 id15b09.x BF907637 601861918 GF582833 AGENCOURT AK083916 Mus muscu

Result No.

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Query Match Length DB

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CNS005NG BZ557685 CF302597 CF338060

311

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RESULT 14
US-10-796-280-12378
US-10-796-280-12378
; Sequence 12378, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; FILE REFERENCE: CL001510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-767-701-27384/c
; Sequence 27384, Application US/10767701
; GENERAL INFORMATION:
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; NAME/KEY: misc_feature
; LOCATION: (1)...(234309)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1. US-10-796-280-12378
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; OTHER INFORMATION: Clone ID: 6858297
US-10-767-701-27384
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CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 27384
LENGTH: 490
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CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 68533
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 12378
LENGTH: 234309
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Best Local Similarity 52.5%;
Matches 62; Conservative
                                                                                                                                                              Matches
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Best Local (
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nuclecic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Sorghum bicolor
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                                                                                                                                                                                             / Match 8.7%;
Local Similarity 51.2%;
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                                                         192 AGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTGGTGGCGCATCT 251
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    282
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Pred. No. 81;
0; Mismatches
                                                                                                                                                              0;
                                                                                                                                                          Score 28.2; DB 6; Length 490; Pred. No. 5.8; 0; Mismatches 63; Indels
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                          GGTGAATCT
GGGCAACCT
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Search completed: April 17, 2004, 20:13:00 Job time : 39.4407 secs

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RESULT 11

US-10-796-280-12417/c

US-10-796-280-12417, Application US/10796280

; Sequence 12417, Application US/10796280

; GENERAL INFORMATION: Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; CURRENT APPLICATION UNMBER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEO ID NOS: 68533
; SOPTMARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12417
; ENOTH: 20618
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; ORGANISM: Drosophila melanogaster
US-10-108-605A-248
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                                                                              ; ORGANISM: Homo sapiens
US-10-796-280-12417
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APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Stam, Lynn
APPLICANT: Stam, Lynn
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REPERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605A
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
    Query Match
Best Local S
Matches 65
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID 0 248
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Local Similarity 51.6%;
hes 65; Conservative
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    Score 28.4; Di
Pred. No. 27;
O; Mismatches
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                                       DB 6;
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      61;
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RESULT 13
US-10-796-280-12452
; Sequence 12452, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHI
; TITLE OF INVENTION: STENOSIS, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-10-796-280-12418
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; ORGANISM: Homo sapiens
US-10-796-280-12418
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US-10-796-280-12452
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STEMOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001510
CURRENT APPLICATION NUMBER: US/10/796,280
CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 68933
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12418
TENORMY 16075
                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/796,280
CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 68533
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12452
LENGTH: 69359
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                                                                                                                                     / Match 8.8%;
Local Similarity 50.0%;
nes 71; Conservative
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Local Similarity 51.6%;
es 65; Conservative
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   GGCAAAGTGGGGATTAGAAACTAGGCAGTTTGACTCCAGAGTCTGTGCCCCTGTCCACTT
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GENETIC POLYMORPHISMS ASSOCIATED WITH
STENOSIS, METHODS OF DETECTION AND USES
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Pred. No. 47;
0; Mismatches
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Pred. No. 39;
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                                                                                                SOFTWARE: Pat
SEQ ID NO 545
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Best Local
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                                                                                                                                          APPLICANT: LUTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEKMANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
FILE REFERENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10/451,467A
CURRENT FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: EP 00870318.3
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: EP 01870003.9
PRIOR FILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2011-01-09
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APPLICANT: Wang, I-Ching
APPLICANT: Major, Michael
TITLE OF INVENTION: METHODS OF TREATING AGE-RELATED DEFECTS AND DISEASES
FILE REFERENCE: 02-1040-A
CHRENEW ADDITION:
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CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: 60/406582
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 60/426068
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10-451-467A-545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CONTRERAS, ROLAND HENRI APPLICANT: EBERHARDT, INES
             TYPE: DNA ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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55.6%; Pred. No. 9.2;
ative 0; Mismatches 44; Indels 0
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Conservative

0; Mismatches Score 28.4; Di Pred. No. 4.9;

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Length 500;

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Query Match 8.8%; Best Local Similarity 50.7%;

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; LENGTH: 500
TYPE: DNA
; ORGANISM: Escherichia coli
PCT-US04-02000-767
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
PCT-US04-02000-767/c
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GENERAL INFORMATION:

APPLICANT: KOVALIC, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38 21 (5535) 8

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                             Sequence 767, Application PC/TUS0402000
GENERAL INFORMATION:
APPLICANT: Science Applications International Corporation
APPLICANT: Transfer Transfer Transfer Transfer Transfer Transfer Transfer Transfer Transfer Transfer
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Best Local Similarity
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SEQ ID NO 21673
LENGTH: 312
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                                                                               SOFTWARE: PatentIn version 3.2 SEQ ID NO 767
                                                                                                                     CURRENT APPLICATION NUMBER: PCT/US04/02000 CURRENT FILING DATE: 2004-01-23 PRIOR APPLICATION NUMBER: US 60/441,745 PRIOR FILING DATE: 2003-01-23 PRIOR FILING DATE: 2003-01-23 PRIOR FILING DATE: 2003-01-23 NUMBER: DS 50/441,806 PRIOR FILING DATE: 2003-01-23 NUMBER OF SEQ ID NOS: 3242
                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Method and System for Identifying Biological Entities in TITLE OF INVENTION: Biological and Environmental Samples FILE REFERENCE: 36609-183264 (SAICO087-PCT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 ACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTTTTTGTTGGACTGG 313
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Pred. No. 9.6;
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Pred. No. 4;
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                                                                                                                                                                                                                                                                                     ; LOCATION: (1)...(35895)
; OTHER INFORMATION: n =
US-10-767-471-10749
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CURRENT FILING DATE: 2004-01-30

NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10749
LENGTH: 35895
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Best Local
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PRIOR FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/478,667
PRIOR FILING DATE: 2003-06-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/789,400 CURRENT FILING DATE: 2004-02-27
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APPLICANT: Buchholz, Ursula
APPLICANT: Skiadopoulos, Mario H.
APPLICANT: Murphy, Brian R.
FITLE OF INVENTION: RECOMBINANT HUMAN METAPNEUMOVIRUS
FILE REFERENCE: 4239-67783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
/15895
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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les 65; Conserv
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, INFORMA
       12662
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           GCCTCTCACCCACTGCTCTTGGGTTTGTCTTGGCAGCAAGAGCCCATCCTCCTGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.4%;
ilarity 49.4%;
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0; Mismatches
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Pred. No. 8.2;
0; Mismatches
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Pred. No. 4.
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                                                                                                                                                                                                                         DB 6;
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APPLICANT: Caou, Yihua
APPLICANT: Caou, Yihua
APPLICANT: Caou, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 5423
LENGTH: 731
TYPE: """
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS132149_1
US-10-767-701-5423
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Query Match
Best Local S
Matches 54
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                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10669
LENGTH: 158027
                                                                                                                                                                                                                                                                                                                                                                     Sequence 10669, Appl GENERAL INFORMATION: APPLICANT: CARGILL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                 APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DET
                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CL001505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Sorghum bicolor
                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)...(15802
                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                      TYPE: DNA
                                                                                           LOCATION: (1)...(158027)
OTHER INFORMATION: n = A, T, C or G, or insertion/deletion polymorphism (see Tables
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 ГССТІВССАТІТІВАССВСАТСЛАСВІТІСВСАВСВАТВСВАТАВАТІСТВАВВАСТІТЛА 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 CATCTCATCATCTTGGAGTTGCGAGTTAGGAGCTGAACCAACTCTCGGGCTG
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53.6%;
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 Score 28.8; D
pred. No. 50;
2; Mismatches
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Pred. No. 4
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                                       DB 6;
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
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Gapop 10.0 , Gapext 1.0
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8.8 2737

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8.8 4507

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(c) 1993 - 2004 Compugen Ltd
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US-10-789-400-36

US-10-767-471-10749

US-10-767-471-10669

US-10-650-609-1

US-10-671-467A-545

US-10-767-701-21673

PCT-US04-02000-767
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Sequence 716, Appl Sequence 10749, Appl Sequence 10749, Appl Sequence 1. Appl Sequence 21673, Appl Sequence 21673, Appl Sequence 21673, Appl Sequence 21417, Appl Sequence 12418, Appl Sequence 12418, Appl Sequence 12418, Appl Sequence 12418, Appl Sequence 12378, Appl Sequence 27384, Appl Sequence 27384, Appl Sequence 1036, Appl Sequence 1036, Appl Sequence 29783, Appl Sequence 2460, Appl Sequence 4553, Appl Sequence 4555, Appl Sequence 4553, Appl Sequence 18, Appl Sequence 18, Appl Sequence 185, Appl Sequence 185, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Sequence 135, Appl Se
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Sequence 40, App.	٠,٠	Sequence 4448, Ap	4447,	Sequence 1/6, Ap	17.5	27	540	144	T/271	18/55,		~	•		e 18171,	e 2/441,	2/293,	0 6 7 4 ,

ALIGNMENTS

NAME/KEY: modified_base LOCATION: (8997)...(89986) OTHER INFORMATION: a, t, c or g FEATURE: NAME/KEY: modified_base LOCATION: (167286)...(167385) OTHER INFORMATION: a, t, c or g US-10-021-698A-716 APPLICANT: KITH, TIM APPLICANT: LITTLE, RANDALL APPLICANT: UND EERDEWEGH, PAUL APPLICANT: UNDUIS, JOSEE APPLICANT: DEL MASTRO, RICHARD APPLICANT: DEL MASTRO, RICHARD APPLICANT: SIMON, JASON APPLICANT: SIMON, JASON APPLICANT: ALLEN, KRISTINA APPLICANT: PANDIT, SUNIL TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: RESPIRATORY DISEASES AND OBESITY FILE REFERENCE: 2976-4044US1 CURRENT APPLICATION NUMBER: US/10/021,698A CURRENT APPLICATION NUMBER: US/10/021,698A CURRENT FILING DATE: 2000-06-14 NUMBER: OS/211,749 PRIOR FILING DATE: 2000-06-14 NUMBER: OS/211,749 RESULT 1 US-10-021-698A-716 S Sequence 716, Application: Query Match Best Local S Matches 65 SOFTWARE: Patentin 2.1 SEQ ID NO 716 LENGTH: 173233 TYPE: DNA ORGANISM: Homo sapiens FEATURE: 200 AGACTCTAACCTTTGGGTCTCATTGCCGTTGCGATTACAGTGGTGGCGCATCTTCTTGGCG 259 1 Similarity 65; Conserv Application US/10021698A Conservative 10.2%; Score 33.2; DB Pred. No. 1.5; 0; Mismatches 0 Q ıΩ DB 6; 53; Length 173233; Indels o ~ ŏ Gaps

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GTCGACGCACCTTGTTGAGCGTTGGCGCCTGGCACCATCGTTTTTGTTGGACTGGTGAA 317 AGAATCTAAGCCTTGACCAAATATGTGTTACTATTACTTTTGTTGTTGTTGTTCTTGC 84547

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GTAACTCCAACCCTCTGCTCGTTGGCCTTGTCACCTCAGTGCTGATTTTGCAGATGAA 84605

84488 260

84548

RESULT

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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & STREET: One filberty Place 46th. Floor CITY: Philadelphia STREET: Oct. Elberty Place 46th. Floor STREET: Oct. Elberty Place 46th. Floor STREET: Oct. Elberty Place 46th. Floor STREET: Oct. Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.00 Place 11.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5110 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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Patent No. 5863724
GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5863724
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5863724ris
STREET: One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: US/08/404,531B
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0003
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
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                                                              CGCAGCAATGCGATAGATCTGAAGACTCT 206
                                                                                                                            GGCAGCTTGGCGATGTCAATGCCATCGATGATGATACGCCCTTCAAACATATCCACCATT
                                                                                                                                                                                                  GGCAAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTT 177
CGGAAAAAGGCGAGAGAGAAGGAGGATTT 4412
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                                                                                                                                                                                                                                                                 ; Score 29.8; DE; Pred. No. 3; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                       Length 5110;
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RESULT 14
US-08-404-531B-5/c
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RESULT 15
US-08-476-900A-4/c
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Ver.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,531B
FILLING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/ACPNT ---
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson,
APPLICANT: Thomas, Gilbert Cote, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:

NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNI
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5863724ris
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LENGTH: 5110 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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                                                                           4440 CGGAAAAAGGCGAGAGAAGGAAGGATTT 4412
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                                                                                                               CGCAGCAATGCGATAGATCTGAAGACTCT
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Pred. No. 3
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                                                                                                                                                                                                                                                                 Length 5110;
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APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 6031150
TITLE OF INVENTION: and Method of Detecting Persistent Hyperinsulinemic Hypoglycer
TITLE OF INVENTION: Infancy
NUMBER OF SEQUENCES: 49

Sequence 4, Application US/08476900A Patent No. 6031150 GENERAL INFORMATION: APPLICANT: Joseph Bryan, Lydia Ac

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; NAME/KEY:
; LOCATION:
US-08-404-531B-27
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US-08-476-900A-27/c
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TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 6031150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Applicat Patent No. 6031150 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                                                                         ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,900A
FILING DATE: 07-UN-1995
CLASSIFICATION: 800
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HYPOTHETICAL: NO
""T-SENSE: NO
""YPE: N-terminal
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                           TELEPHONE: 215-568-310
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 4635 base pair:
                                                                                                              NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BY:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: BY TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One Liberty CITY: Philadelphia
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLE OF INVENTION:
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                        nucleic acid
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215-568-3439
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linear
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           single
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                                                                                                                                                       BYLR-0027
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Pred. No. 2.
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                                                    RAGMENT TYPE: N-terminal
LOCATION:
                  NAME/KEY:
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US-08-476-900A-27
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Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/08/488,546A
FILING DATE: 07-UNE-1995
CLASSIFICATION B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,531
FILING DATE: 15-MARCH-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0026
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6054313
NUMBER OF SEQUENCES:
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                                                                                                                                                      TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela APPLICANT: Thomas, Gilbert Cote, and Robert Gagel TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 4635 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
HYPOTHETICAL:
ANTI-SENSE:
                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 6054313ris
STREET: One Liberty Place 46th. Floor
                                                                          STRANDEDNESS:
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Pred. No. 2.
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CDS 37..4533

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RESULT 9
US-08-232-463-14
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SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 5829
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Patent No. 6660852
GENERAL INFORMATION:
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TITLE OF INVENTION: PROBE FOR DIAGNOSING INFECTIOUS DISEASES
FILE REFERENCE: 19036/33767
CURRENT APPLICATION NUMBER: US/08/809,254A
CURRENT FILLING DATE: 1997-05-16
PRIOR APPLICATION NUMBER: PCT/JP95/02036
PRIOR FILLING DATE: 1995-10-02
PRIOR FILING DATE: 1995-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: JP 236348
PRIOR FILING DATE: 1994-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOR COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                  APPLICATION NUMBER: EP 9: FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             STREET: 100.
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CLASSIFICATION: 435
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NAME: BENT, Stephen A. REGISTRATION NUMBER: 2 REFERENCE/DOCKET NUMBER
                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     DDRESSEE:
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56; Conserv
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ilarity 57.1%;
Conservative
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 NUMBER:
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                                                                                          EP 91 114 300.6
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Pred. No. 1.
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US-08-404-531B-27/c
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US-08-232-463-14
        LIPE: Floppy disk

CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,5315
FILING DATE: 15-MAR-1995
CLASSIFICATION: 415
ATTORNEY/AGENT
NAME:
                                                                                                                                                                                                                                                             Patent No. 5863724

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz

ADDRESSEE: No. 5863724ris

STREET: One Liberty Place 46th. Floor
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GENERAL INFORMATION:
APPLICANT: Joseph
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                CITY: Philadelphia
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                                                                                                                                                                                                                USA
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Thomas, Gilbert Cote, and Robert G
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                                                                              US/08/404,531B
34,293
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                                                                                                                   Version
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US-09-252-991A-13832/c
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Best Local S
Matches 63
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PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13729
                                                        GENERAL INFORMATION:
APPLICANT: GARY L. BIFTON et al.
APPLICANT: GARY L. BIFTON et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 13832
LENGTH: 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
ORGANISM: Acinetobacter baumannii
                                            LENGTH: 1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                         264 ACGCACCTTGTTGAGCGTTGGCGCCTGGCACCATCGTTTTTGTTGGACTGGT 314
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BER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.6%; Score 34.2; DB 4; Length 678; 56.8%; Pred. No. 0.025; tive 0; Mismatches 48; Indels
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Pred. No. 0.023;
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RESULT 7
US-08-961-527-56
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                                                                                                                                                                                                                                                                            NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: BB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 2387 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
TOROLOGY: 11067
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Tocal Similarity
Conserv
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                                                                                                                                                                                        Matches
                                                                                                                                                                                                                      Query Match
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APPLICANT: Charle
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, COMPUTER: HP Vectra 480 OPERATING SYSTEM: MSDOS SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                               9.7%;
Local Similarity 52.7%;
es 68; Conservative
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1082
                                                           1022 GCAATTCAACGGTATTCTCCAAATGAGAAAATTCAAACAGTTAGTCCTTCTGCCTTAAAT 108:
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                                                                                           172 ACGTTTCGCAGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCG
                                                                                                                                             112 TTTGTGGGCAAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCA 171
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                                                                                                                           ATGATTGTG 1090
                                ATTACAGTG
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Pred. No. 0.32;
                                                                                                                                                                                                     Score 31.4; DB
Pred. No. 0.51;
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                                                                                                                                                                                                                      DB 4;
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APPLICANT: EGNERANCHT, NICOLE
APPLICANT: SAHM, HERMANN
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, LOTHAR
APPLICANT: EGGELING, NALTER
ITILE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF
TITLE OF INVENTION: BRANCHED CHAIN ANNO ACIDS, PROCESS FOR THE
TITLE OF INVENTION: 1SOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/265496/MAS
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR PATELING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTMARE: PATENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 1271
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
PEATURE:
TYPE STORE
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US-09-471-803A-1
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; LOCATION: (853)..(1176)
; OTHER INFORMATION: bxnE
; OTHER INFORMATION: ATCC14752
US-09-471-803A-1
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Best Local Similarity 100.
Matches 324; Conservative
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LOCATION: (101)..(853)
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1153
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                                                                                                                                                                                                                                                                                   AAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTTCGC
                                                                                                                             GTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTCGGCACCATCGTT 300
                                                                                                                                                                                                                 AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTG 240
                                                                                                                                                                                                                                                            AAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTTCGC 1032
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                                      TTTGTTGGACTGGTGAATCTTTTC 324
    TTTGTTGGACTGGTGAATCTTTTC 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 324; DB 4; Length 1271;
100.0%; Pred. No. 5e-107;
vative 0; Mismatches 0; Indels 0
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RESULT 3 US-09-471-803A-6

Sequence 13729, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 107196.136
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18

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APPLICANT: KENNERKNECHT, NICOLE
APPLICANT: SAHM, HERMANN
APPLICANT: SAHM, HERMANN
APPLICANT: EGGELING, LOTHAR
APPLICANT: EFEFERLE, WALTER
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR THE EXPORTITLE OF INVENTION: BRANCHED CHAIN ANINO ACIDS, PROCESS FOR TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF FILE REFERENCE: 21123/265496/MAS
CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOSTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 1271
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RESULT 4
US-09-252-991A-13729/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: gene
LOCATION: (853)..(1176)
OTHER INFORMATION: brnE
OTHER INFORMATION: ATCC13032
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LOCATION: (101)...(853)
OTHER INFORMATION: brnF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Corynebacterium glutamicum FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAL INFORMATION:
                                                                                                                                                                   1093
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                                                                                                                          301
                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                    181 AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTG
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                                                                                                               TTTGTTGGACTGGTGAATCTTTTC 324
                                                                                                                                                                                                                                                    AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTG
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Maximum DB
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324
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1 : /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2 : /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
3 : /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4 : /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5 : /cgn2_6/ptodata/2/ina/ETUS_COMB.seq:*
6 : /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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  GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
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  Match
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US-09-252-991A-13832
US-09-252-991A-13832
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US-08-464-531B-47
US-08-464-531B-47
US-08-464-531B-5
US-08-464-531B-1
US-08-464-531B-1
US-08-464-531B-1
US-08-476-900A-1
US-08-476-900A-1
US-08-476-900A-2
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US-08-488-546A-2
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B.6	8.6	8.7	8.7	8.7	8.7		8.8		9.0	9.0	9.0	9.0	9.0	9.1	9.1	9.1	9.1
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Sequence 173, App	Sequence 7, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 74, Appl	Sequence 74, Appl	Sequence 174, App	Sequence 35, Appl	Sequence 15639, A	Sequence 41, Appl	Sequence 345, App	Sequence 343, App	Sequence 342, App	-	Sequence 1, Appli	Sequence 152, App	Sequence 2, Appli	Sequence 2, Appli

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/471,803A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: DE 199 51 708.8
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 324
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE: NAME/KEY: CDS
LOCATION: (1). (324)
COTHER INFORMATION: ATCC14752
US-09-471-803A-4
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US-09-471-803A-4
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APPLICANT: KENNERKSECHT, NICOLE
APPLICANT: SAHM, HERMANN
APPLICANT: EGGELING, LOTHAR
APPLICANT: PFEFFERLE, LOTHAR
APPLICANT: PFEFFERLE, WALTER
TITLE OF INVENTION: WELNICHED CHAIN AMINO ACIDS, PROCESS FOR TITLE OF INVENTION: ISOLATION THEREOF AND USE THEREOF
FILE REFERENCE: 21123/285496/MAS
                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches 324
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Patent No. 6613545
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181
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Similarity 100.0%;
24; Conservative 0
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                                AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTG
                                                                                                                           AAAATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTTCGC
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  AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTTCTCATTGCCGTTGCGATTACAGTG
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Pred. No. 2.4e-107;
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RESULT 14
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                                                                                                                                                                                                                 20-DEC-2001; 2001JP-00387059.

20-DEC-2001; 2001JP-00387131.

20-DEC-2001; 2001JP-00403299.

20-DEC-2001; 2001JP-00403300.

27-SEP-2002; 2002JP-00327515.
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                                                          Single nucleotide polymorphism sites in barley varieties and DNA sequences containing them for analysis and identification of bar varieties and production of barley transformants with desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA clone originating in barley containing SNP encoding sequence #10859.
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17-OCT-2003
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67; Conserv
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nilarity 53.6%;
Conservative
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Disclosure;

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20-DEC-2001;
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gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 392 BP; 100 A; 105 C; 85 G; 102 T;
                                              Single nucleotide polymorphism sites in barley varieties and sequences containing them for analysis and identification of varieties and production of barley transformants with desired
                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare;
                                                                                                                                                                                                                                                                                                                                                                                                    DNA clone originating in barley containing SNP encoding sequence #10909.
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17-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACL20918;
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                                                                                                                                                                                                                                                           16-DEC-2002;
                                                                                                                                                                                                                                                                                                                WO2003057877-A1.
                                     characteristics.
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                                                                                                   2003-587127/55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Conserv
                                                                                                                                                      UNIV JAPAN OKAYAMA.
                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTTGGCACCATCGTTTTTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTGGTGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; DNA; 470
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                                                                                                                             Takeda
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2001JP-00403299.
2001JP-00403300.
2002JP-00327515.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(first entry)
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                                                                                                                                                                                                                                   2001JP-00387059.
                                                                                                                                                                                                                                                                                                                                                                               nucleotide
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                                                                                                                             Kohara
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                                                                                                                                                                                                                                                                                                                                                                              polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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Pred.
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No. 1.
                                                                                                                                                                                                                                                                                                                                                                               SNP;
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                                                                                                                                                                                                                                                                                                                                                                               genotype-phenotype analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ď,
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XX 29-SEP
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XW Human;
XW MHC cl
XW MOC cl
XW MOC cl
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Best Local S
Matches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; major histocompatibility complex class II transactivator; MHC class II transactivator; antisense modulation; immunosuppressive; antimicrobial; antidiabetic; antitheumatic; antiarthritic; cytostatic; nootropic; neuroprotective; immunostimulant; autoimmune disorder; MHC Class II transactivator inhibitor; infection; transplant rejection; diabetes; rheumatoid arthritis; cancer; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACF39600 standard; cDNA; 6672
  The present invention describes a compound (I) that is 8-50 nucleobases in length: (a) targets a nucleic acid molecule encoding major histocompatibility complex (MHC) class II transactivator, and specifically hybridises with the nucleic acid encoding the MHC class II transactivator; and inhibits the expression of MHC class II transactivator; or (b) specifically hybridises with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding MHC class II transactivator. (I) has immunosuppressive, antimicrobial, antidiabetic, antirheumatic, antiarthritic, cytostatic, nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple sclerosis; severe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                New antisense oligonucleotides for modulating MHC class II transactivator gene expression, particularly useful for treating autoimmune disorders such as transplant rejection, Alzheimer's disease, or multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-DEC-2002; 2002WO-US038616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bennett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003050247-A2.
                                                                                                                                                                                                                                                                                        Example 13; Page 93-99; 129pp; English.
                                                                                                                                                                                                                                                                                                                                              or infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-DEC-2001; 2001US-00006366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-577294/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dobie KW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  II transactivator encoding cDNA SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=  a
/product= "MHC class II transactivator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220
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Pred. No. 5.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease; gene; ss
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ACL2025/G
ID ACL20
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AC ACL20
XX DNA C
DT 17-OC
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KW Barle
KW Gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6672 BP; 1392 A; 1954 C; 1868 G; 1458 T; 0 U; 0 Other:
                                                                                                                                                                                                                                                                                                                                                                   20-DEC-2001; 2001JP-00387059.

20-DEC-2001; 2001JP-00387131.

20-DEC-2001; 2001JP-00403299.

20-DEC-2001; 2001JP-00403300.

27-SEP-2002; 2002JP-00327515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barley; single nucleotide polymorphism; SNP;
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17-OCT-2003
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                                                                                                   Single nucleotide polymorphism sites in barley varieties and DNA sequences containing them for analysis and identification of bar varieties and production of barley transformants with desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                             cytostatic;
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                                                                                                                                                                                                                                                                                                                                        cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
h; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
atic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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2000US-0209531P.
2000US-0233133P.
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2000US-0234009P
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Young PE, Soppet DR, Augustus M, Weaver Z; Carter S, Ebner ø Endress Ó Horrigan

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing agent to be tested for anti-neoplastic activity, and of the expression of a gene of a signature gene set. g.cells to a chemical determining a change

Claim 1; SEQ ID NO 6458; 44pp; English.

The present invention describes a method (M1) for screening for an anticone populatic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises in indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an activity and can be used in gene therapy. M1 can be used for screening an complexitic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result composerties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, carcinoma, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, concer, infiltrating doublar cancer, squamous cell carcer, infiltrating doublar cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's

Sequence 6672 BP; 1392 A; 1954 Ç 1868 <u>.</u> 1458 ;; 0 U; 0 Other;

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RESULT 9
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Best Local S
Matches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3144 BP; 1056 A; 676 C; 680 G; 732 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                           Sequences AAS59506-AAS59804 represent DNA molecules encoding propionibacterium across immunogenic polypeptides. The proteins and associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. across. The disorders in the disorders in the disorders in the disorders in the disorders in the disorders.
                                                                                                                                                                                                                                                        Propionibacterium acnes vaccinating against and treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-APR-2001; 2001WO-US012865.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes immunogenic protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS59515 standard; DNA; 66788
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     L'maisonneuve
                                                                                                                                                                                                Claim 1; SEQ ID NO 10; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTAAATTTCTATATATTAGTTAAATATGATGTTATTAATGTTTACCTTGATATCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACAGTCTTATGTTTĞTTĞĞ 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCACCATCGTTTTGTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Persing DH,
e J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteopathic; neuroprotectant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.1%;
                                                                                                                                                                                                                                                                                         polypeptides and nucleic acids useful for diagnosing infections, especially useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitcham ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     JL, Wang SS,
, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bhatia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                       for
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include their

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

Claim 1; SEQ ID NO 10; 1481pp; English

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RESULT 10
ACF64444/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). This sequence encodes the polypeptides shown in AAU41313-42019 and AAU67473. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      particularly involved in the inflammatory lesions associated with acine vulgaris. A method for detecting the presence or absence of P. acines in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein the proteins of the invention and determining the amount of bound protein the proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is all infections of bone, joints and the central nervous system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACF64444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 66788 BP;
                                                                                                                         Mitcham JL, Skeiky YAW, Pe
Zhang Y, Wang S, Jen S, I
Barth B, Vallieve-Douglass
                                                                                                                                                                                                                                                          11-OCT-2002;
                                                                                                                                                                                                                                                                                           24-APR-2003
                                                                                                                                                                                                                                                                                                                        WO2003033515-A1
                                                                                                                                                                                                                                                                                                                                                     Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                    Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes DNA contig sequence #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACF64444 standard; DNA; 66788 BP
                                                                                                                                                                                                                          15-OCT-2001; 2001US-00978825
                                                                                            WPI; 2003-381789/36.
                                                                                                                                                                                           (CORI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
71; Conserv
                                                                                                                                                                                           CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCATTCTGATCGCGGCGACGAACCGCCCCGACGTTCTTGACCCGGCTCTGCTACGTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAAGGTTCACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTCTCATTGCCGTTGCGATTACAGTGGTGGCGCATCTTCTTGGCGGTCGACGCACCTTG
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                                                                                                                                                                                                                                                          2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13534 A; 21369 C; 19347 G; 12530 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        joints and the central nervous system, however it ed in the inflammatory lesions associated with acne
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                                                                                                                                            Persing DH,
Lodes MJ,
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Pred. No. 13
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                                                                                                                                                                                                                                                                                                                                                                                         vaccine; ds.
                                                                                                                                            Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                              Maisonneuve JL;
Jones R, Carter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U; 8
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coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lywine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office

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RESULT 7
ADA71938 s
XX
ADA71938;
AC
ADA71938;
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ADA71938;
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DT
20-NOV-200
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Plant; bac
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Matches 324;
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                                       Identifying at least pathogenic infection bacterial, fungal or
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F, Quan S,
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S, Tao
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                                           one gene involved in plant resistance or response
for conferring resistance or tolerance to a plant
viral infection by determining or detecting plant
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Pred. No. 2.1e-99;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                        Sequence 2000 BP; 336 A; 265 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                       illustrate the invention.
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                                                                                                                    AMTCAKCKYKNAMTKWWTTWACAWRATSWRWARAMAGMRWKRYKMKRAYWWRWWRCWKAGW
                                                                                                                                                   CTCCGGGCGGTTCCTTAATCCTTAAGCCCCTACGTGAATCACAATTTGTGGGCAAA
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AATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTA
                                                          ATGGCGATGTGGATGCCAGCAGGAATCCTTGCCATTTTGACCGCATCAACGTTTCGCAGC
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                                                                                                                                                                                                                                                           10.7%;
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RESULT 8
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AC ABL27130;
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11-JUL-2000;
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2000US-00614150
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                                                    This invention describes a novel isolated polynucleotide (I) containing CC at least one sequence that (i) is 70% identical with a sequence that CC encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) cC or (5); (iii) encodes a polypeptide at least 70% identical with (3) cC or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least CC or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least CC or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least CC or (5); (iv) are sequences of 753 bp (2) or 324 bp (4); (b) cC or contains at least CC one or more (I), where these are replicative DNA; (c) production of CC one or more (I), where these are replicative DNA; (c) production of CC branched-chain l-aa by fermentation of coryneform bacteria in which the CC branched-chain l-aa by fermentation of coryneform bacteria in which the CC branched-chain l-aa by fermentation of coryneform bacteria being CC used for fermentative production of branched-chain the branched-chain amino acids, CC specifically overexpressed; and (d) method for isolating the branched coryneform bacteria being CC used for fermentative production of branched-chain amino acids, cc specifically leucine, isoleucine and valine, which are useful in medicine CC probes for isolation of related sequences. Transformation with (I) CC increases yield of branched-chain amino acids. This sequence encodes the CC corynebacterium glutamicum ATCC 13032 brnF and brnB proteins described in two
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0 Other

The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from

Claim

7; SEQ ID NO 1; 246pp + Sequence Listing; English.

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07-APR-2000;
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Tateishi
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                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
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acid synthesis; ds.
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Ozaki A;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid array useful for Corynebacterium glutamicum during from Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUN-2001; 2001DE-01028510
                                                                                                            C. glutamicum
                                                                                                                                     05-SEP-2001
                                                                                                                                                                                      AAH21109
                                      Corynebacterium glutamicum
                                                                          coryneform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Loca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                              nutrition; ds
                                                                          acid production; brnF;
orm bacterium; leucine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGCTCCGGGCGGTTCCTTAATCCTTAAGCCCCCTACGTGAATCACAATTTGTGGGC
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                                                                                                                                                                                        standard; DNA; 1271
                                                                                                                                                                                                                                                               TTTGTTGGACTGGTGAATCTTTTC 324
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                                                                                                                                     (first entry)
                                                                                                            DNA encoding brnF and brnE.
 Location/Qualifiers 101. .856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 324; DB 7; )
Pred. No. B.8e-101;
Mismatches 0;
                                                                           brnE; branched-chain amino acid;
isoleucine; valine; medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monitoring mRNA expression of fermentation, comprising nucleic
                                                                                                                                                                                                                                                   324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel isolated polymucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that CC encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) cC polypeptides; (ii) encodes a polypeptide at least 70% identical with (3) cC or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least 15 consecutive bases from (1)-(ii). The invention also describes (a) cc protein derived from sequences of 753 bp (2) or 324 bp (4); (b) cc coryneform microorganisms, especially Corynebacterium, transformed with 0 coryneform microorganisms, especially Corynebacterium, transformed with 0 cone or more (I), where these are replicative DNA; (c) production of 0 coryneform bacteria in which the 0 brnE and/or brnF genes (or equivalent sequences) are amplified, 0 cc especially overexpressed; and (d) method for isolating the brnE and/or 0 brnF genes. (I) is used for transformation of coryneform bacteria being 0 used for fermentative production of branched-chain amino acids, 0 cc especially leucine, isoleucine and valine, which are useful in medicine 0 cc protes for isolation; (I) can also be used as source of primers and 0 cc protes for isolation of related sequences. Transformation with (I) cc increases yield of branched-chain amino acids. This sequence encodes the 1 crowners of the invention of the proteins described in the corynebacterium glutamicum ATCC 14752 brnF and brnE proteins described in 1 crowners of 1 corynebacterium glutamicum ATCC 14752 brnF and brnE proteins described in 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1 crowners of 1
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Best Local Sim
Matches 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4 (i); Page 13; 23pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New export
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kennerknecht N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1271 BP;
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P-PSDB; AAB86247, AJ
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(KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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GTGGCGCATCTTCGTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCGCTGGCACCATCGTT
                                                                              AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGGATTACAGTG
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                                                    AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes from coryneform bacteria, useful for increasing ve production of branched-chain amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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853. .1179
/*tag= b
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/product= "brnE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 324; DB 4;
Pred. No. 1.6e-100;
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Best Local Similarity
Matches 324; Conserv
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                                                                                             16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                              Nakagawa
Tateishi
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                                                                                                                                                                                                                                 Corynebacterium
                                                                                                                                                                                                                                                           Coryneform bacterium; amino organic acid synthesis; ds.
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                                                                                                                                                                                                                                                                                                 coding sequence fragment SEQ ID NO:
                                                                                              99JP-00377484.
2000JP-00159162.
2000JP-00280988.
                            Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
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Pred. No. 8.8e-101;
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                                                                                                                                                                                                                                                                          synthesis; vitamin; saccharide;
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RESULT 3
ACAO1970
ID ACAO
XX ACAC
XX ACAC
XX ACAC
XX COX

nucleic acid array;

fermentation; 1961.

glutamicum

13-JUN-2001; 2001DE-01028510

DE10128510-A1 Corynebacterium Coryneform;

19-DEC-2002

04-JUN-2003 ACA01970;

(first entry)

glutamicum

derived ORF SEQ ID

ACA01970

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Best Local Simi
Matches 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-376931/40.
P-PSDB; AAG90036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID NO 290; 246pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 324 BP; 60 A; 79 C; 80 G; 105 T; 0 U; 0 Other;
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                      TTTGTTGGACTGGTGAATCTTTTC
                                                                      GTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTT
                                                                                                                                               AGCAATGCGATAGATCTGAAGACTCTAACCTTTGGTCTCATTGCCGTTGCGATTACAGTG
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                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 2000000000
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324
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Gapop 10.0 , Gapext 1.0
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1: geneseqn1980s:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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This invention describes a novel isolated polynucleotide (I) containing at least one sequence that (i) is 70% identical with a sequence that encodes at least one of 251 amino acid (aa) (3) or 108 aa (5) polypeptides; (ii) encodes a polypeptide at least 70% identical with (3) or (5); (iii) is the complement of (i) or (ii), or (iv) contains at least 15 consecutive bases from (i) -(1ii). The invention also describes (a) protein derived from sequences of 753 bp (2) or 324 bp (4); (b) coryneform microorganisms, especially Corynebacterium, transformed with one or more (I), where these are replicative DNA; (c) production of

Claim 5; Page 16; 23pp; German.

New export genes from coryneform bacteria, useful for increasing fermentative production of branched-chain amino acids.

WPI; 2001-391595/42. P-PSDB; AAB86248. Kennerknecht N,

Eggeling L,

Sahm H,

Pfefferle W;

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Acl20924 DNA clone		DNA	_	DNA C	DNAC				Ac120861 DNA clone			Pro	Ac120863 DNA clone			Ent			cion (, c	

ALIGNMENTS

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RESULT 1
AAH21111
AAH21111 standard; DNA; 324 BP
                                                                                                                                                                                                                                 L-amino acid production; brnF; coryneform bacterium; leucine; animal nutrition; ds.
                                                                                                                                                                                                                                                            C. glutamicum brnE DNA.
                                                                                                                                                                                         02-MAY-2001.
                                                                                                                                                                                                       EP1096010-A1.
                                                                                                                                                                                                                   Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                            05-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                          AAH21111;
                                                                                                                                                              27-OCT-1999;
                                                                                                                                                                          11-OCT-2000; 2000EP-00122057.
                                                                                                                                        (DEGS ) DEGUSSA AG.
(KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
                                                                                                                                                              99DE-01051708
                                                                                                                                                                                                                                         brnE; branched-chain amino acid;
isoleucine; valine; medicine;
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gene SGS

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TLYSSATIFVYPSIYEGFGIPPLEAIACGAPILLSDIEVFREIGNVAEFFSPLNAKE
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Pred. No. 2.4;
0; Mismatches 133;
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AX120085 AX114121
AX120085.1 GI:14036800
                                                                                                                                   Campylobacter fetus
Campylobacter fetus
Bacteria; Epsilonproteobacteria;
Bacteriaplobacteraceae; Campylobacter.
1 (bases 1 to 65865)
Blaser,M.J. and Gotschlich,E.C.
                                                                                                                                                                                                                                                   AIZLIZDY

65865 bp DNA linear BCT 21-APR-2003
Campylobacter fetus strain 23D sap gene locus, partial sequence.
AY211269 AF027405 J05577 L15800 S44580 S76860
AY211269.1 GI:28974206
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patent: EP 1108790-A 1 20-JUN-2001;
KYOWA HAKCO KOGYO CO., LTD. (JP)
Location/Qualifiers
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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Yokoi, H., Tateishi, N., Senoh, A., Ik
2 (bases 1 to 65865)
Blaser,M.J. and Gotschlich,E.C.
Surface array protein of Campyl
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/db xref="taxon:1718"
/note="seq 1 to long (3.309.400) split in 11,
0.000.001 0.349.980 349.980"
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mol_type="genomic DNA"
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 of Campylobacter fetus. Cloning and
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Pred. No. 1.1e-88;
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Ikeda, M. and Ozaki, A.
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J. Biol. (
91035477
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Dworkin,J., Tummuru,M.K. and Blaser,M.J.
A lipopolysaccharide-binding domain of the Ca
S-layer protein resides within the conserved
of silent and divergent homologs
J. Bacteriol. 177 (7), 1734-1741 (1995)
95204338
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5 (base
                                                                                                                                                                                                                         Submitted (03-JAN-2003) Microbiology and Medicine, New York University School of Medicine, VAMC ROOM 6006W 423 E. 23rd Street, New York, NY 10016, USA On or before Mar 15, 2003 this sequence version replaced gi:255285, gi:4403445, gi:144211, gi:289533, gi:913763.
                                                                                                                                                                                                                                                                                                                                                               Submitted (30-SED-1997) Division of Infectious Diseases, University, A-3310 MCN, Nashville, TN 37232, USA 10 (bases 1 to 65865)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (20-MAY-1993) Division of Infectious Diseases,
University School of Medicine, Nashville, TN 37232, USA
9 (bases 1 to 65865)
Thompson, S.A., Shedd, O.L., Ray, K.C., Beins, M.H., Jorgens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tummuru, M.K. and Blaser, M.J.
Rearrangement of sapA homologs with conserved and in Campylobacter fetus
Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7265-7269 (
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Tummuru,M.K. and Blaser,M.J.
Characterization of the Campylobacter fetus sapA promoter: evidence that the sapA promoter is deleted in spontaneous mutant strains J. Bacteriol. 174 (18), 5916-5922 (1992)
                                                                                                                                                                                                                                                                                                                           10 (bases 1 to 65865)
Tu,Z.-C., Wassenaar,T.M., Thompson,S.A. and Blaser,M.J
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                  Blaser, M.J.
Direct Submission
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Tu,Z.C., Wassenaar,T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type I secretion system J. Bacteriol. 180 (24),
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                                                                                                                                                        /organism="Campylobacter fetus"
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/strain="23D"
                                        gene="mtfA"
note="Cf0001"
                                                                                      'gene="mtfA"
                                                                                                                       db_xref="taxon:196"
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Shedd,O.L.,
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/product="MINA gyrase (topoisomerase II) B subunit"
/db_xref="G1:2132770"
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TIGRO1058:parE Gpos: DNA topoisomerase IV,
TIGRO1059:gyrB: DNA gyrase, B subunit"
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PF01751:Toprim domain
PF02518:Histidine kinase-, DNA gyrase B-, phytochrome-like
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Similarity 100.0%;
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TTTGTTGGACTGGTGAATCTTTTC
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                                                                                               Corynebacterium glutamicum ATCC 13032
Corynebacterium glutamicum ATCC 13032
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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Corynebacterium glutamicum ATCC
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                                              Nakagawa, S
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This sequence is conducted by collaboration of Kyowa Co. Ltd. And Kitasato University.
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2292. 3476
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PF02768:DNA polymerase III beta subunit, C-terminal
'IIGR00663:dnan: DNA polymerase III, beta subunit"
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|strain="ATCC 13032"
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Asahi-machi, Machida,
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REFERENCE AUTHORS TITLE

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                                                                                                                                                      Rennerukunehito, N., Sahm, H., Eggering, L. and Pfefferle, W.

Nucleotide sequence encoding the discharge of branched amino acid,
method of isolating the same and utilization thereof
patent; JP 2001169788-A 4 26-JUN-2001;
DEGUSSA HUELS AG, FORSCHINGSZENTRUM, JUELICH GMBH
OS COTYNEDACTERIUM Glutamicum ATCC13032
PN 2001159788-A/4
PD 26-JUN-2001
PF 24-OCT-2000 JP 2000324315
PR 24-OCT-1999 DE 19951708.8
PI NICOLE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, WALTER PI
PFEFFERLE
PC C12N15/09, C07K14/34, C12N1/21, C12P13/06, C12P13/06, C12R1:15),
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PC C12N15/00, C12R1:15)
CC brnP
CC C12N15/00, C12R1:15)
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   100.0%; llarity 100.0%; Conservative 0;
                                                                              /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                               Location/Qualifiers
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encoding
the same
     Score 324; DB 6;
Pred. No. 5.8e-89;
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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.

1 (bases 1 to 2105)
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Corynebacterium glutamicum BrnE regulator (lrp) genes, complete
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Export of L-isoleucine from Corynebacterium glutamicum:
two-gene-encoded member of a new translocator family
J. Bacteriol. 184 (14), 3947-3956 (2002)
22077265
                                                                                                                                                                                                                                                                                                                                                                Submitted (07-NOV-2001) IBT-1, Juelich 52425, Germany
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Kennerknecht, N., Egg
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/db_xref="taxon:1718"
complement (385..711)
/gene="brnE"
           complement (708.
/gene="brnF"
complement (708.
                                                                         /product="BrnE"
/product="BrnE"
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/db_xref="G1:21311380"
/ta_nsel="MTTDFSCTLLVVAVCAVITFALRAVPFLILKPLRESQFVGKMAM
/translation="MTTDFSCTLLVVAVCAVITFALRAVPFLILKPLRESQFVGKMAM
WMPAGILAILTASTFRSNAIDLKTLTFGLIAVAITVAHLLGGRRTLLSVGAGTIVFV
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/transl_table=
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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Nucleotide sequences coding for branched-chain amino
proteins, method for isolating them and their use
Patent: EP 1096010-A 6 (02-MAY-2001;
Degussa AG (DE) ; PORSCHUNGSZENTRUM JUELICH GMBH (DE)
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wwpagilailfastfrsnaidlktltfgliavaitvvahilggrrtllsvgagtivfv
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Kennerikunehito, N., Sahm, H., Eggering, L. and Pfefferle, W. Nuclectide sequence encoding the discharge of branched ami method of isolating the same and utilization thereof Patent: JP 2001169788-A 1 26-JUN-2001;

DEGUSSA HUELS AG, FORSCHUNGSZENTRUM JUELICH GMBH OS COTYNEBACTEVIUM GILLAMICUM ATCC14752

PN JP 2001169788-A/1

PD 26-JUN-2001

PF 24-OCT-2000 JP 200324315

PR 27-OCT-1999 DE 19951708.8

PI INICOLE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, P
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NICOLE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, WALTER
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/db_xref="taxon:32644"
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Kennerknecht, N., Sahm, H., Eggeling, L. and Pfefferle, W.

Nucleotide sequences coding for the export of branched chain
acids, process for the isolation thereof and use thereof
patent: US 6613545-A 1 02-SEP-2003;
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                                                                    i (bases 1 to 1271)
Kennerknecht,N., Sahm,H., Eggeling,L. and Pfefferle,W.
Nucleotide sequences coding for the export of branched chain
acids, process for the isolation thereof and use thereof
Patent: US 6613545-A 6 02-SEP-2003;
Location/Qualifiers
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Sequence 1 :
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AX137709.1
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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Nucleotide sequences coding for branched-chain am
proteins, method for isolating them and their use
Patent: EP 1096010-A 1 02-MAY-2001;
Degussa AG (DE); FORSCHUNGSZENTRUM JUBLICH GMBH
Location/Qualifiers
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Nucleotide sequence encoding the discharge of branched amino
method of isolating the same and utilization thereof
patent: JP 2001169788-A 3 26-7UN-2001;

DEGUSSA HUELS AG, FORSCHUNGSZENTRUM JUELICH GMBH
OS COTYNEDACTERIUM GlUTANICUM ATCC14752

PN JP 2001169788-A/3

PD 26-JUN-2001

PP 2001169788-A/3

PD 27-OCT-2000 JP 2000324315

PF 24-OCT-2000 JP 2000324315

PF 27-OCT-1999 DE 19951708.8

PI NICOLE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, WALT
PFEFFERLE

PC C12N15/09, C07K14/34, C12N1/21, C12P13/06, C12P13/06, C12P13/06

PC (C12N15/09, C12R1:15), (C12N1/21, C12R1:15), (C12P13/06, C12P13/06,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
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Nucleotide sequence
method of isolating
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                                         TTTGTTGGACTGGTGAATCTTTTC 324
                                                                                                      GTGGCGCATCTTCTTGGCGGTCGACGCACCT
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24-OCT-2000 JP 2000324315
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NICOLE KENNERUKUNEHITO, HERMANN SAHM, LOTHAR EGGERING, WALTER
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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18 Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
Yokoi,H., Tateishi,N., Senoo,A., Ikeda,M. and Ozaki,A.

Novel polynucleotide
Patent: JP 2002191370-A 290 09-JUL-2002;

KYOWA HAKKO KOGYO CO LITD

KYOWA HAKKO KOGYO CO LITD

SCOTynebacterium glutamicum
PN JP 2002191370-A/290

PD 09-JUL-2002

PP 15-DEC-2000 JP 2000405096
PI SATOSHI NAKAGAWA,HIROSHI MIZOGUCHI,SEIKO ANDO,MIKIO HAYASHI,
PI KEIKO CCHIAI,
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TTTGTTGGACTGGTGAATCTTTTC
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(C12N1/21,C12R1:13),(C12N1/21,C12R1:01),(C12P13/08,C12R1:15),
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Patent: ED 1108790-A 290 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium glutamicum
Corynebacterium glutamicum
Corynebacteria; Actinobacteridae; Actinomycetales;
Bacteria; Actinobacteria; Actinobacteridae; Corynebacterium.
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Sequence 290 from
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/mol_type="genomic
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                                                                                                                                                                                                                                         /organism="Corynebacterium glutamicum"
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/db_xref="taxon:1718"
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Mismatches
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Pred. No. 5e-89;
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Degussa AG (DE) ; FORSCHUNGSZENTRUM JUELICH GMBH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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Sequence 4 from Patent EP1096010.

AX137712
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      GTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTT
                        GTGGCGCATCTTCTTGGCGGTCGACGCACCTTGTTGAGCGTTGGCGCTGGCACCATCGTT
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Conservative 0
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. 18 the number of results predicted by chance to have a

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SUMMARIES

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JOURNAL	Tittle	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AR391955	RESULT 1
Patent: US 6613545-A 4 02-SEP-2003;	Nucleotide sequences coding for the export of braithied chain amino acids, process for the isolation thereof and use thereof	Kennerknecht, N., Sahm, H., Eggeling, L. and Pietterie, W.	1 (bases 1 to 324)	Unclassified.	Unknown.	Unknown.		AR391955.1 GI:40115726	AR391955	Sequence 4 from patent US 6613545.	AR391955 324 bp DNA linear PAT 18-DEC-2003		

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MEDLINE=22709201; PubMed=12810954;

Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P.,

Bell M., Droege M., Fartmann B., Fischet H.-P., Ge Z., Hoerster A.,

Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,

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Helicobacter hepaticus.";

Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906 (2003).

EMBL; AE017146; AAP73077.1;

Hypothetical protein; Complete proteome.

Hypothetical protein; Complete proteome.
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Matches 68
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Q93KB4;
                              pump EmrAB.";
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ410307; CAC44347.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:00003700; Fitranscription factor activity; IEA.
GO; GO:00003700; Fitranscription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0006810; F:transport; IEA.
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Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Welch R.A., Burland V., Dinukett G. III, Redford P., Roesch P.,

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

EMBL; AE016765; AAN81687.1;

PIR; C85916, C85916.
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GO; GO:0006810; P:transport; IEA.
InterPro; IPR004471; AziC.
Pfam; PF03591; AziC; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 245 AA; 26093 MW; 20AAF2D91E644
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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          InterPro; IPR004471; AzlC
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5093 MW; 20AAF2D91E644DB3 CRC64;
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Pfam; PF03591; AzIC; 1.
PROSITE; PS00043; HTH_GNTR_FAMILY; 1.
NON TER
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SEQUENCE 247 AA; 26103 MW; 895810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I., Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A., Utterback T., Rizzo M., Lee K., Kosack D., Moesti D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
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                                                                                                                                                                                                 Complete proteome. SEQUENCE 230 AA;
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InterPro; IPR004471; AzlC.
Pfam; PF03591; AzlC; 1.
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE016783; AAN67998.1; -. TIGR; PP2385; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 GLEFALCSLFVTLTLDSCRTKKQ-IPSLLLAGLSFTIALVVIPGQALFAALLIFLG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 GLTDEVFAAATÄRLARDNRRWŚEPWMLGVALSAWLSWVAGTVIGAVFRNGPLEGYPAVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 ALIDEAYAVTAARPA----GWSAWRLISMQIAFHSYWVFGGLTGVAI----AELIPFEIK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 IIYAGASQFVITALLSAGASIWVAALTVMAMDVRHVLYGPSLRRRIMQRLPTGKTAWWAF 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 VSPSKAALEPDDKGYRRYEIAQGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSG
   29 RYEIAQGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVV 88
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                                                                      59;
                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microbiol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALAFMLPALFISFILASFRRRQSLVVAAALGGACIGLIVSSIP----
                                                                                                                                                                                                 230 AA; 24752 MW; 32C878FCDC403A81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
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                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              4:799-808 (2002)
                                                                                              15.3%;
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                                                                  43;
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                                                                                                  Score 194; DB 16; Length 230; Pred. No. 7.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8958101295841B73 CRC64;
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                                                                      Mismatches 101;
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89 GAAPLGAIALTTLLVNFRHVFYAFSFPLHVVKNPIA-RFYSVFALIDEAYAVTAARP-AG

6 ROAFLHGATAILFLSLAVAFWGLLAGSMATEANLSAWQGQGLSATVFAGAAQLVATGMLK 65

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RESULT 10
QBDVS9
ID V99
ID QBDVS
AC QBDVS
DT 01-Mp
DT 01-Mp
DT 01-Mp
DT 01-NC
CS SMU.
CS SKTE
COC Bactre
CC NCB:
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RESULT 11
Q8X908
ID Q8X90
AC Q8X90
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Best Local S
Matches 70
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01-MAR-2003
01-MAR-2003
01-OCT-2003
  Q8X908;
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STRAIN-MAIS / ARCC 700610 / Serotype C;

MEDLINE-22295063; PubMed=12397186;

Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S.,

Li S., Zhu H., Najar F., Lai H., White J., Roe BA., Ferretti

Li S., Zhu H., Najar F., Lai H., White J., Roe BA., Ferretti

"Genome sequence of Streptococcus mutans UA159, a cariogenic o
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InterPro; IPR000437; Prok_lipoprot_S.
Pfam; PP03591; AzlC; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
COMPLETE PROCEOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE014886; AAN58144.1; -.
GO; GO:0016021; C:integral to membrane;
GO; GO:0006810; P:transport; IEA.
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SMU.388.
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                                                                                                                                                                                                                                                                                 191
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                                                                                                                                                                                                                                  MFVSIFESQLAAMMQFVKLKKIGLILLAVTLSYFL-LVIVISESLAVLLSTLIGCFAGVL
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                                                                                                                                           LDVR
                                                                                                                                                                                                                                                                               LFVTL----TLDSCRTKKQIPSLLLAGISFTIALVVIPGQALFAALLIFLG-----L
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                                                                                                                                                                                        LTIR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 AA;
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(Trembirel. 23, Last sequence update)
(Trembirel. 25, Last annotation update)
tegral membrane protein, possible branched-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acad. Sci. U.S.A. 99:14434-14439(2002).
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                             PRELIMINARY;
                                                                                                                                           232
                                                                                                                                                                                                                                                                                                                                                                         ----Pagwsawrlismqiafhsywvfggltgvalaelipf-eikglefalcs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.8%; Score 200.5;
28.7%; Pred. No. 2.20
tive 44; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91;
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                                                                                                                                                                                                                                  228
RESULT 12
Q8FEQ6
ID Q8FEQ
AC Q8FEC
DT 01-MA
DT 01-MA
DT 01-JC
DE HYDOT
DE HYDOT
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Best Local
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
01-JUN-2003 (TrEMBLrel. 2
Hypothetical protein yga7
YGAZ OR C3235.
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SEQUENCE
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"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.", Nature 409:529-533(2001).
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MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe 1
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag
Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli
"Complete genome sequence of enterohemorrhagic Toba 10157.H7 and genomic comparison with a laboratory strain K-12.";
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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01-MAR-2002 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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PIR; H91071; H91071.

GO; GO:0016021; C:integral to membrane;

GO; GO:0006810; P:transport; IEA.

InterPro; IPR004471; AzlC.

Pfam; PF03591; AzlC; 1.
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Z3983 OR ECS3544.
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EMBL; AE005497; AAG57791.1; -.
EMBL; AP002562; BAB36967.1; -.
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STRAIN=0157:H7 / F
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MEDLINE=21074935; PubMed=11206551;
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Pred. No. 3.6e-08;
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Matches 64
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MEDLINE=22294977; PubMed=12381787;
Schell M.A., Karmirantzou M., Snel B., Vil
Pessi G., Zwahlen M.-C., Desiere F., Bork
Pridmore R.D., Arigoni F.,
"The genome sequence of Bifidobacterium lo
to the human gastrointestinal Frace"
                                                                                                                                                                                                                                                                                                                             Q8Y223 PRELIMINARY; PRT;
Q8Y223
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequ
01-UN-2003 (TrEMBLrel. 24, Last anno
Hypothetical transmembrane protein RS
RSC0513 OR RS04992.
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Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

EMBL; AE014801; AAN25456.1; -

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR004471; AzlC.

Pfam; PF03591; AzlC; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 338 AA; 37538 MM; 805D6F54BA0C80A5 CRC
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Bifidobacteriaceae; Bifidobacterium.
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SEQUENCE FROM N.A.

STRAIN-GMI100;

MEDIINE-21681879; PubMed=11823852;

MEDIINE-21681879; PubMed=11823852;

Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot Salanoubat M., Ghoisne N., Claudel-Renard C., Cunnac S., Demans Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demans Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
                                                                                                                                                                                                                NCBI_TaxID=305;
                                                                                                                                                                                                                                                          Ralstonia solanacearum (Pseudomonas solanacearum)
Bacteria; Proteobacteria; Betaproteobacteria; Bur
Burkholderiaceae; Ralstonia.
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%; Pred. No. 2.6e.
37; Mismatches
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805D6F54BA0C80A5 CRC64;
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ork P., Delley
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y M.,
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Schiex T.,
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9**7** 81

LLTTFFITSRHFLYSVSMRSKIAPLPLKWRLSLGFLLTDELFAI---

AGHHSDEQFNR

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ALTTLLVNFRHVFYAFSFPLHVVKNPIA-RFYSVFALIDEAYAVTAARPAG-----WSA

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RESULT 9
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Best Local S
Matches 57
                                                                                                                                                                                                     SEQUENCE FROM N.A.

C STRAIN=RIMD 2210633 / Serotype O3:K6;

C STRAIN=RIMD 2210633 / Serotype O3:K6;

X MEDILINE=22508454; PubMed=12620739;

X Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagon A., Makino K., Oshima M., Nakano M., Yamashita A., Kubota Y., Kin Ijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kin A., Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

A yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic med distinct from that of V. cholerae.";

I Lancet 36:1743-3749(2003).

IL Lancet 36:1743-3749(2003).

IL Lancet 36:1743-3749(2003).

R EMBL, AP005085; BAG61873.1; T. membrane; IEA.

R GO; GO:0006810; P:transport; IEA.

R GO; GO:0006810; P:transport; IEA.

R GO; GO:0006810; P:transport; IEA.

R GO; GO:0006810; P:transport; IEA.

R GO; GO:0006810; P:transport; IEA.

R GO; GO:0006810; P:transport; IEA.

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R GO; GO:0006810; P:transport; IEA.

R GO; GO:0006810; P:transport; IEA.

R GO; GO:0006810; P:transport; IEA.

R GO; GO:0006810; P:transport; IEA.

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EMBL; AL646059; CAD14041.1; -...

GO; GO:0016021; C:integral to men

GO; GO:0006810; P:transport; IEA.

InterPro; IPR004471; AzlC.

Pfam; PF03591; AzlC; 1.

Hypothetical protein; Complete pi
SEQUENCE 242 AA; 25196 MW; F7
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Vibrionaceae; Vibrio.
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  21
                                                  44 LGMYPIGIA---FGLLVIQYGYEWWAAPL----FSGLIFAGSTEMLVIALVVGAAPLGAI
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Pred. No. 4.7e-09;
8; Mismatches 95
                                                                                                          Score 203.5; 1
Pred. No. 1.3e
14; Mismatches
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C STRAIN-Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;

C MEDLINE=22120827; PubMed=12125824;

X MEDLINE=22120827; DubMed=12125824;

X MARTINEZ-ARIAS R., Henne A., Hartsch T., Merkl R., Schmitz R.A.,

RA Brueggemann H., Lienard T., Christmann A., Baeumer S., Jacobi C.,

RA Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,

RA Fritz H.-J., Gottschalk G.;

RA Fritz H.-J., Gottschalk G.;

RT Transfer between Bacteria and Archaea.";

RT Transfer between Bacteria and Archaea.";

Mol. Microbiol. Biotechnol. 4:453-461(2002).

DR MOJ. MCGrobiol. Biotechnol. 4:453-461(2002).

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0016810; P:transport; IEA.

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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Branched-chain amino acid transport protein.
AZIC OR MM3262.
Marhanonari
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EMBL; AE011050; AAM06804.1; -.
GO; GO:0016021; C:integral to
GO; GO:0006810; P:integral to
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Pfam; PF03591; AzlC; 1.
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ilarity 32.6%;
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Pred. No. 2.4e-16;
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MEDLINE=21145866; PubMed=11248100;
May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Ki
"Complete genomic sequence of Pasteurella multocida Pm70.";
proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AB006078; AAK02506.1; ...
GO; GO:0006810; Pittansport; IEA.
GO; GO:0006810; Pittansport; IEA.
InterPro; IPR004471; AzlC.
Pfam; PF03591; AzlC: 1.
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Pasteurellaceae; Pasteure
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                                                                                                                                                                                                                                                                                                                                      SGRQIFYGISMLEKYGAYLGKK---RWYLISTLVDEAFSLNYMAKVPEGIERGWYFFFVS
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                                                                                                                                          IAPHSYWVFGGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDS-CRTKKQIPSLLLAGLS 215
FTALLVVGKTYFILPTLIGIWFALTLRRVKLSAKLAK
                                            FTIALVVIPGOALFAALLIFLGLLTIRYFFL-GKAAK
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ilarity 31.3%;
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Pred. No. 3.9e-15;
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Last annotation update)
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Pred. No. 2.7e-11;
1; Mismatches 94;
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL/, AP005224; BAC19736.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR004471; AzlC.
Pfam; PF03591; AzlC; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 238 AA; 25739 MW; 02BDDED0BAB33A31 CRC64;
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STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

Kawarabayasai Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,

Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,

Usuda Y., Sugimoto S.;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence up
01-JUN-2003 (TrEMBLrel. 24, Last annotation
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Bacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
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                                                                                                                               LLLAGLSFTIALVVIPGQALFAALLIFLGLLTIRY 243
                                                                                                                                                                                       GTRLLTLQIVCQSLWVFPGIIGAVAGQALPDGLKGMEFALTALFVVLAWEAFTNNKDWSL 186
                                                                                                                                                                                                                                            AWRLISMQIAFHSYWVFGGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDSCRTKKQIPS
                                                                                                                                                                                                                                                                                                    VGPFSAL-VTGFMVNFRHIFYGLTFPRNAIRSKVGRAYSTYALTDEAYAIASARPPGEIS
                                                                                                                                                                                                                                                                                                                                                     AAPLGAIALTTLLVNERHVFYAFSFELHVVKNPIARFYSVFALIDEAYAVTAARPAG-WS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRYFFLGKAAK 251
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                                                                          PLTAVVLALLAGFLAPGOMLVLALTAYFVILLFRF
                                                                                                                                                                                                                                                                                                                                                                                                                   EIGGGIRETSAVGLGLVPLGLAFGLLMVQSGYAWWWTPIFSIVIYAGSMEYLAIGLIAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.3%; Score 448.5; DB llarity 42.3%; Pred. No. 3e-28; Conservative 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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QBNL66
               RRAP RRAPA
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Best Local
SEQUENCE FROM N.A.

STRAIN=C2A / ATCC 35395 / DSM 2834;

MEDLINE=21929760; PubMed=11932238;

Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

FitzHugh W., Calvo S., Engels R., Smittov S., Atnoor D., Brown A.,

FitzHugh W., Calvo S., Engels R., Smittov S., Atnoor D., Brown A.,

Allen N., Maylor J., Stange-Thomann N., DeArellanto K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A.,

Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            o1-JUN-2002 (TREMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation updat
Branched chain amino acid transport protein Azlc.
MA3437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSTKHO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genomic sequence of Corynebacterium Submitted (MAY-2002) to the EMBL/GenBank/DDBJ EMBL, APO05283; BACC0477.1; -. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0006802; P:transport; IEA. InterPro; IPR004471; AzlC.
Pfam; PF03591; AzlC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBNL66;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UTM-2003 (TrEMBLrel. 24, Last annotation update)
Predicted branched-chain amino acid permease (azaleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
SEQUENCE 237 AA; 25867 MW; 193EB1182E0CF923 CRC64;
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                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                   Methanosarcina acetivorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGL3083
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2214;
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es 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 AWRLISMQIAFHSYMVFGGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDSCRTKKQIPS 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIRGGIGETLTVGLGLIPLGLAFGLLMVQTGFAWWWTPIFSFVIYAGSMEFLAIGMVTAG
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Pred. No. 1.2
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                             SPTREMBL 25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-608-504-3
1269
1 MQKTQEIHSSLEVSPSKAAL......LLIFLGLLTIRYFFLGKAAK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        April 16, 2004, 06:51:17; Search time 49.6407 Seconds (without alignments) 1595.367 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
sp_plant:*
sp_vicus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_bacteriap:*
                                                                                                                                                 sp_organelle:*
sp_phage:*
                                                                                                                                                                                                     invertebrate:*
_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1017041
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	* Query Match Length	DB	Π	Description
1 !	1269	100.0	251	16	08AILA8	Q8ntp8 corynebacte
N	448.5	35.3	238	16	8MS480	Q8fsw8 corynebacte
w	428.5	33.8	237	16	Q8NL66	Q8nl66 corynebacte
4,	301	23.7	291	17	Q8TKH0	Q8tkh0 methanosarc
Uī	285	22.5	244	17	Q8PS25	Q8ps25 methanosarc
ወ	237	18.7	240	16	Q9CNK7	Q9cnk7 pasteurella
7	214	16.9	338	16	Q8G3T5	Q8g3t5 bifidobacte
00	209	16.5	242	16	Q8Y223	Q8y223 ralstonia s
9	203.5	16.0	236	16	Q87IS6	Q87is6 vibrio para
10	200.5	15.8	232	16	QBDVS9	Q8dvs9 streptococc
11	198	15.6	245	16	806X8Ö	Q8x908 escherichia
12	198	15.6	245	16	SQEFEGE	Q8feq6 escherichia
13	197	15.5	247	N	Q93KB4	Q93kb4 erwinia chr
14	194	15.3	230	16	Q88KAS	Q88ka5 pseudomonas
15	194	15.3	231	16	Q7VI98	Q7vi98 helicobacte
16	194	15.3	245	16	Q83JZ6	Q83jz6 shigella fl

45	44	43	42	41	40	ω 9	38	37	36	35	34	ω ω	32	31	30.1	29	28	27	26	25	24	23	22	21	20	19	18	17
161	161	161.5	163	163.5	166	167	167	168	169	174.5	174.5	175	175	176	176.5	176.5	177	177.5	181	181	181.5	181.5	182	184.5	184.5	185	186	192
12.7	•	•	•	12.9	•	13.2	13.2		•		•	•	13.8	•	•	•	٠	•		4	٠.	4.	٠	4.	4	4.	14.7	Ů,
224	224	230	238	219	235	230	230	241	235	237	235	257	252	261	242	235	233	218	239	234	256	241	241	237	237	230	237	250
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Q8FYL5	Q8VW59	Q8CQK2	Q92NN2	Q8XGA3	Q92BR4	80XQ8	Q8E2V7	QBCUI8	19448D	Q9K8U2	Q9CF68	Q8ZBX0	Q91276	Q88T22	Q98KC6	Q831J7	611880	Q97T14	Q9KKU8	Q8UGF6	Q92R05	Q81FC0	Q81SD8	Q7WB32	Q7WMJ8	Q8EG49	Q8D6G0	QBREQB
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Chloride channel protein 4 (ClC-4).
CLCN4 OR CLCN4-2 OR CLC4.
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MEDLINE=95400329; PubMed=7670496;
Rugarli E.I., Adler D.A., Borsani G., Tsuchiya K., Franco Hauge X., Disteche C., Chapman V., Ballabio A.;
"Different chromosomal localization of the Clcn4 gene in M and C57BL/6J mice.";
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                            Mus musculus (Mouse)
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transepithelial transport.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the chloride channel fami
SIMILARITY: Contains 2 CBS domains.
                                           . Genet. 10:466-471(1995).
FUNCTION: Voltage-gated chloride channel. Chloride channels have several functions including the regulation of cell volume; membrane potential stabilization, signal transduction and
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> V (IN VS ANTIGEN).
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SMART; SM00116; CBS; ;
Ionic channel; Ion tra
Voltage-gated channel;
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InterPro; IPRO01807; C1-Channel_volt.
Pfam; PF00571; CBS; 2.
Pfam; PF00654; voltage_CLC; 1.
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MGD; MGI:104571; Cl
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                                                                                                                   EAYAVTAARPAGWSAWRLISMQIAFHSYWVFGGLTGVAIAELIPFEIKGLEFALC-SLFV
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                                              RCNIAWCRRRKTTRLGRYPVLEVIAVTAVTAIVAYP
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April 16,
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25.6%;
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            2004, 06:53:44
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25; Mismatches
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CBS domain; Repeat.
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MEDLINB=91058522; PubMed=2123099;
MEDLINB=91058522; PubMed=2123099;
Avent N.D., Ridgwell K., Tanner M.J.A., Anstee D.J.;
Avent N.D., Ridgwell K., Tanner M.J.A., Anstee D.J.;
"CDNA cloning of a 30 kDa erythrocyte membrane protein associated with Rh (Rhesus) -blood-group-antigen expression.";
with Rh (Rhesus) -blood-group-antigen expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND VARIANTS THR-153; GLU-232 AND VAL-237. KRAShiwase K., Ishikawa Y., Uchikawa M.; "The serological profile and molecular basis of the RhE variants (RhEFM and RhEKH) in Japanese."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-16.
MEDLINE=88294325; PubMed=3135863;
Bloy C., Blanchard D., Dahr W., B
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                                                                                                                                               VARIANTS BLOOD GROUP C AND E.
WEDLINE=94035121; PubMed=8220426;
Mouro I, Colin Y, Cherif-Zahar B., C
"Molecular genetic basis of the human
Nat. Genet. 5:62-65(1993)
                                                                                                                                                                                                                                                                                                                                           "Determination of the N-terminal sequence of human red polypeptide and demonstration that the Rh(D), (c), and are carried by distinct polypeptide chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Protein-sequence studies on Rh-related polypeptides suggest the presence of at least two groups of proteins which associate in the human red-cell membrane."; Biochem. J. 256:1043-1046(1988).
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Avent N.D., Ridgwell K., Mawby W.J.,
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                                                                                                                                                                                                                            "Organization of the gene (RHCB) encoding the human blood group RhCcBe antigens and characterization of the promoter region."; Genomics 19:68-74(1994).
                                                                                                                                                                                                                                                                 Cherif-Zahar
Colin Y.;
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MEDLINE=94245182; PubMed=8188244;
Charif-Zahar B., le van Kim C., Rouillac C., Raynal V., Cartron J.-P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSUE=Bone marrow;
                                                                         FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMERANE. SUBCCELULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=4:
Name=Put.
      Name=RHVI;
IsoId=P18577-3;
                                             Name=RHIV
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                                 IsoId=P18577-2;
                                                         IsoId=P18577-1;
     Sequence=VSP_005702, VSP_005705;
                                                         Sequence=Displayed;
                              Sequence=VSP_005703,
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Uchikawa M.;
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n Rhesus blood
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(E) antigens
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LINES EXPRESSING

ISOId=P18577-4; Sequence=VSP 005701;
TISSUE SPECIFICITY: RESTRICTED TO TISSUES OR CELL LINES EXPRESS
EXTHROID CHARACTERS.

POLYMORPHISM: RhCE and RhD are responsible for the RH blood gr.
system. The molecular basis of the ErRh3/erRh5 blood group
antigens is a single variation in position 225; pro-225
corresponds to Rh3 and Ala-225 to Rh5. The molecular basis of
c=Rh2/c=Rh4 blood group antigens is a single variation in posi
102; Ser-102 corresponds to Rh2 and pro-102 to Rh4.
SIMILARITY: BELONGS TO THE RH FAMILY. STRONG, TO RHD. s of the position group

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EMBL; M34015; AAA36557.1; -...

R EMBL; X54534; CAA38401.1; -...

R EMBL; X54534; CAA38401.1; -...

R EMBL; X53095; CAA44801.1; -...

R EMBL; X63096; CAA44810.1; -...

R EMBL; X63096; CAA44810.1; -...

R EMBL; X63096; CAA44812.1; -...

R EMBL; X63096; CAA44812.1; -...

R EMBL; X63096; CAA44812.1; -...

R EMBL; X63096; CAA44812.1; -...

R EMBL; X63096; CAA44812.1; -...

R EMBL; X63096; CAA44812.1; -...

R EMBL; X63096; CAA44812.1; -...

R EMBL; X63096; AAA33928.1; -...

R EMBL; X63096; AAA3928.1; -...

R EMBL; X63096; AAA3928.1; -...

R EMBL; X63096; AAA3928.1; -...

R EMBL; X63096; AAA3928.1; -...

R EMBL; X63096; AAA4812.1; -...

R EMBL; X63096; AAA4812.1; -...

R EMBL; X63096; AAA4812.1; -...

R EMBL; X63096; AAA4812.1; -...

R EMBL; X63096; AAA4812.1; -...

R EMBL; X63096; CAA44812.1; -...

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R EMBL; X63096; CAA44812.1; -...

R EMBL; X63096; CAA44812.1; -...

R EMBL; X63096; AAA1812.1; -...

R EMBL; X63096; AAA1812.1; -...

R EMBL; X63096; AAA1812.1; -...

R EMBL; X63096; AAA1812.1; -...

R EMBL; X63096; AAA1812.1; -...

R EMBL; X63096; AAA1812.1; -...

R EMBL; X63096; AAA1812.1; -...

R EMBL; X63096; AAA1812. Transmembrane; transp; 1. Blood group antigen; Alternative

splicing;

31 31 96 144 191 222 222 237 317 317 416 353 267 416 40 35 POTENTIAL.
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POTENTIAL.
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POTENTIAL.
POTENTIAL. Missing (in isoform RHIV) /FTId=VSP_005704. MISSING (In 1806orm RHVI).
/FTIG-VSF_005702
VCCNRVLGIHISVMHSIFSLLGLLGEITYIVLLVLHTVWN
-> DWLPGPPQHWGTQLGHRNSSHVWSPDRFAPXSQNMEST Missing (in isoform RHVIII). /FTId=VSP_005701. IGFQVLLSIGELSLAIVIALTSGLLTGLLLNLKIWKAPHVA
KYFDDQVFWKFPHLAVGF -> FAPKSQNMESTSC (in /FTId=VAR_006912. Q -> R (IN C(W)/RH8 ANTIGEN) FTId=VAR 006911. rsoform RHVI) FTId=VSP_005703 FTId=VAR_006913 _005705. RHIV).

FTId=VAR_006914

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P51793, O9UBU1;
01-OCT-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
7-10-ide channel protein 4 (ClC-4).
                                                                                                  [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
MEDLINE=20035030; PubMed=10564087;
MEDLINE=20035030; PubMed=10564087;
MEDLINE=20035030; PubMed=10564087;
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94348498; PubMed=8069296;
van Slegtenhorst M.A., Bassi M.T., Borsani G., Wapenaar M.C.,
Perrero G.B., de Conciliis L., Rugarli E.I., Grillo A., Franco B.,
Zoghbi H.Y., Ballabio A.;
Tagene from the Xp22.3 region shares homology with voltage-gated
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Mammalia; Eutheria;
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Primates;
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Best Local S
Matches 40
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P18577; Q02163; Q02164; Q02165; Q16160; Q9UEC2; Q9UEC3;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Blood group Rh(CE) polypeptide (Rhesus C/E antigens) (Rh30A) (RhIXB)
(Rh polypeptide 1) (RhPI).
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MMM; 302910; -.

GO; GO:0005247; F:voltage-gated
GO; GO:0006810; P:transport; TAX

InterPro; IPR000644; CBS domain.

InterPro; IPR001807; C1-Channel
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Pfam; PF00654; voltage CLC; 1.
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EMBL; AB019432; BAA77327.1;
EMBL; AF170492; AAD50981.1;
PIR; I37242; I37242.
                                Cherif-Zahar B., Bloy C., le van Kim C., Blanc Hermand P., Salmon C., Cartron J.-P., Colin Y. "Molecular cloning and protein structure of a
                                                                                         TISSUE=Bone marrow;
MEDLINE=90349591; P
                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
polypeptide."
Proc. Natl. A
                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL
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                                                                                             PubMed=1696722;
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U.S.A. 87:6243-6247(1990

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RESULT 12
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Pfam; PF00654; Voltage_CLC; 1.
PRINTS; PR00762; CLCHANNEL.
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InterPro; IPR001807; C1-channel_volt.
MEDLINE=98289612; I
Lu R., Schuster V.I
"Molecular cloning
                                              SEQUENCE FROM N.A.

MEDLINE=96379664; PubMed=8787677;

LU R., Kanai N., Bao Y., Schuster V.L.;

"Cloning, in vitro expression, and tissue prostaglandin transporter cDNA(hPGT).";

J. Clin. Invest. 98:1142-1149(1996).
                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SM00116; CBS;
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-1998 (Rel. 37, Last sequence update)
-2003 (Rel. 41, Last annotation update)
-carrier family 21 member 2 (Prostaglandin transporter)
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hPGT: gene organization, promoter activity, and chromosomal localization.";
Biochem. Biophys. Res. Commun. 246:805-812(1998).
Biochem. Biophys. Res. Commun. 246:805-812(1998).
In control of the community of the sease of newly synthesized prostaglandins from cells, the transporthelial transport prostaglandins, and the clearance of prostaglandins from circulation. Transports PGD2, as well as PGE1, PGE2 and PGINGLIGHT. Integral membrane protein.
ITISSUE SPECIFICITY: Ubiquitous.
ITISSUE SPECIFICITY: Ubiquitous.
                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Query Match Best Local S Matches 58 GO; GO:0005824; C:integral to plass GO; GO:0005824; C:membrane fractio GO; GO:0005829; F:lipid transporte GO; GO:0006869; F:lipid transport; InterPro; IPR004157; OATP Cterm. InterPro; IPR004157; OATP Cterm. InterPro; IPR004156; OATP Nterm. CARBOHYD CARBOHYD SEQUENCE TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM Transmembrane; TRANSMEM 2 TRANSMEM 7 TRANSMEM CARBOHYD Pfam; PF03137; OATP C; Pfam; PF03132; OATP N; TIGRPAMS; TIGR00805; oa PROSITE; PS50850; MFS; L; AF056722; AAC62004.1; L; AF056723; AAC62004.1; L; AF056724; AAC62004.1; L; AF056725; AAC62004.1; L; AF056725; AAC62004.1; L; AF056726; AAC62004.1; L; AF056728; AAC62004.1; L; AF056728; AAC62004.1; AF056729; AAC62004.1; L; AF056729; AAC62004.1; L; AF056729; AAC62004.1; L; AF056731; AAC62004.1; L; AF056731; AAC62004.1; 178 40 LAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFA----HGNC:10955; Similarity LLAGIGTVPIQ-PFGISYVDDFSEPSNSPLYISILFAISVFGPAFGYLLGSIMLQIFVDY 49: 643 7.8%; ilarity 22.6%; Conservative Ä Transport; C:integral to plasma membrane; TAS. C:membrane fraction; TAS. F:lipid transporter activity; TAS. P:lipid transport; TAS. 491 · 70116 MW; 192 230 278 348 386 386 531 531 134 oat; 1. Glycoprotein.
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RESULT 10
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Chloride channel protein 5
CLCN5 OR CLC5.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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SUBCELLULAR LOCATION: Integral membrane protein.
TISSUB SPECIFICITY: Kidney specific.
SIMILARITY: Belongs to the chloride channel family.
SIMILARITY: Contains 2 CBS domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Voltage-gated chloride channel. Chloride channels several functions including the regulation of cell volume; membrane potential stabilization, signal transduction and
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246
317
428
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; Transmembrane; CB
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                                                                                                                                                                                                                                                                                    Chloride channel; Chloride;
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RESULT 11
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Chloride channel protein 5 (ClC-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                       MEDLINE=96215316; PubMed=8626585;
Sakamoto H., Kawasaki M., Uchida S., Sasaki S., Marumo F.;
"Identification of a new outwardly rectifying Cl- channel that
belongs to a subfamily of the ClC Cl- channels.";
J. Biol. Chem. 271:10210-10216(1999).
                                                                                                                                                                                                                                                                                                                                                                                 Steinmeyer K., Schwappach B., Bens M., "Cloning and functional expression of related to kidney disease.", J. Biol. Chem. 270:31172-31177(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLC5_RAT
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96125100; PubMed=8537381; Steinmeyer K., Schwappach B., Bens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                             Biol. Chem. 271:10210-10216(1996).

FINCTION: Voltage-gated chloride channel. Chloride channels have FUNCTION: Voltage-gated chloride channel. Chloride channels have several functions including the regulation of cell volume; membrane potential stabilization, signal transduction and transepithelial transport. May play an important role in renal tubular function.

SUBJECTIONAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Ridney specific.

SIMILARITY: Belongs to the chloride channel family.

SIMILARITY: Contains 2 CBS domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
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POTENTIAL.
POTENTIAL.
CBS 1.
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Pred. No. 1.1
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Sciurognathi; Muridae; Murinae; Rattus.
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EMBL outstation -
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cions on its
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MEDIINE-86121370; PubMed-8575751;
Fisher S.E., van Bakel I., Lloyd S.E., P.
Thakker R.V., Craig I.W.;
"Cloning and characterization of CLCN5,"
"Cloning and characterization of CLCN5,"
                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE-97402204, PubMed=9259268;
Lloyd S.E., Guenther W., Pearce S.H.S., Thomson A., Bianc Bosio M., Craig I.W., Fisher S.E., Scheinman S.J., Wrong Jentsch T.J., Thakker R.V.;
"Characterisation of renal chloride channel, CLCN5, mutat hypercalciuric nephrolithiasis (kidney stones) disorders. Hum. Mol. Genet. 6:1233-1239(1997).
-i- FUNCTION: Voltage-gated chloride channel. Chloride ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96158876; PubMed=8559248;
Lloyd S.E., Pearce S.H.S., Fisher S.E., Steinmeyer K., Schwappach B., Schelnman S.J., Harding B., Bolino A., Devoto M., Goodyer P., Rigden S.P.A., Wrong O., Jentsch T.J., Craig I.W., Thakker R.V.;
"A common molecular basis for three inherited kidney stone diseases.", Nature 379:445-449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Expression of CLCN voltage-gated chloride channel genes in human blood vessels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Aortic endothelium, and Vascular smooth MEDLINE=99222497; PubMed=10198195; Lamb F.S., Clayton G.H., Liu B.-X., Smith R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95179126; PubMed=7874126; Fisher S., Black G.C.M., Lloyd S.E., Thakker R.V., Craig I.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    channel gene implicated in Dent nephrolithiasis).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS NPHL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thakker R.V., Craig I.W.;
"Isolation and partial characterization of a chloride channel which is expressed in kidney and is a candidate for Dent's dis (an x-linked hereditary nephrolithiasis).";
Hum. Mol. Genet. 3:2053-2059(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 487-746 FROM
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                                                                                                                                                                         SUBCELIULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Kidney. Moderately expressed in aortic
vascular smooth muscle and endothelial cells, and at a sligh
higher level in the coronary vascular smooth muscle.
DISEASE: Defects in CLCN5 are a cause of X-linked recessive
hypophosphatemic rickets (XIRM) [MIM:300008].
DISEASE: Defects in CLCN5 are the cause of idiopathic low
molecular weight proteinuria of japanese children (JILP)
renal failure.

DISEASE: Defects in CLCN5 are the cause of X-linked recessive

nephrolithiasis type 1 (NPHL1) [MIM:310468]; also designated XRN.

NPHL1 is characterized by hypercalciuria, nephrocalcinosis, renal
                                                                                   [MIM:300008].

DISEASE: Defects in CLCN5 are the cause of X-linked recessive nephrolithiasis type 2 (NPHL2) [MIM:300009]; also known as Dent disease. NPHL2 is a renal form of Fanconi syndrome, characterized by hypercalciuria, nephrocalcinosis, renal stones and progressive
                                                                                                                                                                                                                                                                                                                                           FUNCTION: Voltage-gated chloride channel. Chloride channels several functions including the regulation of cell volume, membrane potential stabilization, signal transduction and transepithelial transport. May play an important role in ren
                                                                                                                                                                                                                                                                                                                             tubular function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLCK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cardiol. 31:657-666(1999)..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLU-506 AND PRO-520,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hatchwell E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pearce
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                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 muscle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ë
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutations
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                                                                                                                                                                                                                                                                                                                                                 in renal
                                                                                                                                                                                                                                                                         slightly
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S

27

Conservative

ω 3

Mismatches

68;

Indels

75;

Gaps

86 10;

YRRYEIAQGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIAL

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Query Match
Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X91906; CAA63000.1; -
EMBL; X81836; CAA57430.1; -
PIR; 137277; 137277.
Genew; HGNC:2023; CLCN5.
MIM; 300008; -..
MIM; 310468; -..
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00571; CBS; 2.
Pfam; PF00654; voltage_CLC;
PRINTS; PR00762; CLCHANNEL.
                                                                                                                                                                                                                                                                          TRANSMEM
TRANSMEM
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Ionic channel; Ion to
Voltage-gated channe
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005887; C:integral to plasma membrane; TAGO; GO:0005254; F:chloride channel activity; TAS.GO; GO:0007588; P:excretion; TAS.GO; GO:0006810; P:txansport; TAS.InterPro; IPR001807; CBS_domain.
                                        SEQUENCE
                                                                     VARIANT
                                                                                          VARIANT
                                                                                                                       VARIANI
                                                                                                                                           VARIANT
                                                                                                                                                                VARIANT
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                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stones and renal insufficiency, but differs from Dent that the patients lack urinary acidification defects, osteomalacia.
SIMILARITY: Belongs to the chloride channel family.
SIMILARITY: Contains 2 CBS domains.
                                                                                                                                                                                                                                                                                                                                                                                 mutation.
          Similarity
                                        746
                                                                                                                                                                                                                                                                  527
                                                                                          520
                                                                                                                        512
                                                                                                                                           506
                                                                                                                                                                280
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                                                                                                                                                                                                                          57
                                                                                                                                                                                                                                                                                                                                                                                         channel;
                                        AA
/
                                                                                                                                                                                                                                                                                                                                                                                                    transport;
                                                                                                                                           506
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209
266
337
372
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         8.0%;
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                                        MW;
                                                    Currents).

/FTId=VAR 001621.

S -> P (in NPHL2).

/FTId=VAR 001622.

E -> D (in NPHL2; abolishes t)

E -> D (to NPHL2; abolishes t)
                                                                                                                    / FTId=VAR (1 NPHL2).

/ FTId=VAR (001617.

S -> L (1 NTARH).

/ FTId=VAR (001618.

R -> P (1 NPHL1).

/ FTId=VAR (001619.

G -> E (1 NPHL1).

/ FTId=VAR (001620.

-- R (1 NPHL2; all (1 NPHL2).
         Score 101.5; D
Pred. No. 0.92;
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POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
POTENTIAL.
                                                  currents; total
/FTId=VAR_001623
                                                                                                                                                                                                                                                                              POTENTIAL
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                                                                                                                                                                                                                 FTId=VAR
                                                                                                                                                                                                                                     FTId=VAR
                                                                                                                                                                                                              FTId=VAR 001615.
-> V (in NPHL2).
FTId=VAR 001616.
                                         EF913C5BA40C85D8 CRC64;
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                    DB
                   1;
                                                                                                                        abolishes
                   Length
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                    746;
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RESULT 8
NU4C_PSINU
ID NU4CP
AC Q8WHZ
AC 28-FEB
DT 28-FEB
DT 28-FEB
DT 28-FEB
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Best Local S
Matches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00146; N
PROSITE; PS00667
PROSITE; PS00668
Oxidoreductase; I
TRANSMEM 29
TRANSMEM 129
TRANSMEM 129
TRANSMEM 348
TRANSMEM 348
TRANSMEM 348
TRANSMEM 372 A
28-FEB-2003
28-FEB-2003
28-FEB-2003
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=IAM M-101;
Takahashi Y., Shonai F.,
Matsubara H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D01014; BAA00814.1; -.
PIR; JQ2135; JQ2135.
InterPro; IPR001694; Resp_NADH_dh1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure of a co-transcribed gene cluster, ndhl-frxB-nd cloned from the filamentous cyanobacterium plectonema boy plant Cell Physiol. 32:969-981(1991).

-I- FUNCTION: NDH-1 shuttles electrons from NAD(P)H, via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plastoquinol.
SUBCELUTLAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: Belongs to the complex I subunit I family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient (By similarity). CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P)(+)+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sulfur (Fe-S) centers, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species is believed to be plastoquinone. Couples the redox reaction to proton
                                                              PSINU
                                                                                                                                                                     214
                                                                                                                                                                                                    224
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                                                                                                                                                                                                                                                                                                                              131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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PS00667; COMPLEXI ND1 1; FALSE NEG.
PS00668; COMPLEXI ND1 2; 1.
                                                                                                                                                                      LSFTIALVVIPG------QALFAALLIFLGLLTIRYFFL
                                                                                                                                                                                                                                                                                                                                                                                           DVVPAKA-----DK------LLFTLGPAIVVIPVFLSY--LILPFGQNLQITDVGL
                                                                                                                                                                                                                                                                                                                                                                                                                       EVSPSKAALEPDDKGYRRYEIAQGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFS
                                                                                                                                                                                                                                                                                                                            GI-----FLWIAL-SSVVPIGLLMSGYASNNKYSLLGGLRAAAQSISYEL-----PLA
                                                                                                                                                                                                                                                                                                                                                            GLIFAGSTEMLVIALVVGAAPLGAIA-----LTTLLVNFRHVFYAFSFPLHVVKNPIA 124
                                                                                                                                        WEFPISLSVISGLIGVPESTPWLQLIFAT--IGIGMTLLKAYFL
                                                                                                                                                                                                    LAECERIPFDLPEAEEELVAGYQTEYSGMKFALFYLGSYVNLTLSAL----LFAVLYLGG
                                                                                                                                                                                                                                                               --LSVLAVVMSNSLSTVDIVNQQAGYGI-----LGWNIWR---QPVGFIIFWI----AA
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(Rel. 41, Created)
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                                                              STANDARD;
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119
151
276
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370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     39;
 sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 110.5; DB Pred. No. 0.096; 9; Mismatches
                                                                                                                                                                                                                                   -EIKGLEFALCSI--FVTLTLDSCRTKKQIPSLLLAG
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                                                              498
                                                              Å
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lectonema boryanum.";
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    BAPPRB
 CLC5 HUMAN
P51795;
01-OCT-1996
01-OCT-1996
15-MAR-2004
Chloride chai
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(Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 43, Last annotation update)
(annel protein 5 (ClC-5).

STANDARD;

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Query Match
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Matches 69
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HAMA; MF 00491; -; 1.
InterPro; IPR003918; NADHub oxred4.
InterPro; IPR001750; Oxidored_q1.
Iffam; PF00361; oxidored_q1; 1.
PRINTS; PR01437; NUOXDRDTASE4.
Oxidoreductase; NAD; NADP; Quinone; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for constitutions as long as its content of the constitutions as long as its content of the constitutions as long as its content of the constitutions as long as its content of the constitutions as long as its content of the constitutions as long as its content of the constitutions as long as its content of the constitutions as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as lo
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P)(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wakasugi T., Nishikawa "Complete nucleotide se Psilotum nudum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Moniliformopses; Psilotophyta; Psilotales; Psilotaceae; Psilotum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Kingyoku;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement
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                                                                         240
                                                                                                                                                                                                                                                                                                        286
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406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 VVGAAPLG--------AIALTTLIVNFRHVFYAFSFPL-HVVKNPIARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L Similarity
69; Conserv
                                                                                                                                                                                                                                                                                                    VQIAYASLISFSLPNIKRRIAYSSVSHMGFVIIGISSITDIGTNGAILQMISHGLIGAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGMY--PIGIAFGLLVIQYGYEW------WAAP--LFSGLIFAGSTEMLVIAL
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nce of the chloroplast
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; C65048; C65048.
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.am; PF0359; AZIC; 1.
.ypothetical protein; Transport; Transmembrane; Complete protein; PF0359; ASIC; 1.
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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       SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049943; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F.
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                                                                                                                                                                   NCBI_TaxID=2234;
                                                                                                                                                                                                           Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeog
Archaeoglobaceae; Archaeoglobus
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(Rel. 40, Last annotation updat
L protein AF1755.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMBL outstation of the EMBL outstation on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the hyperthermophilic, reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000982; AAB89495.1;
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIGR; AF1755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; B69469; B69469.
                                                                     102
                                                                                                       126
                                183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pro; IPR004471;
PF03591; AzlC;
158
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Similarity 24.2%;
56; Conservative 4
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                                GLEFALCSLFVTLTLDSCRTKKQIPSLLLAGLSFTIALVVIPGQALFAALL
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1 protein;
14 37 55
123 14
155 17
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57
143
175
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Transport; Transmembrane;
34 POTENTIAL.
57 POTENTIAL.
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                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                      Score 145; DB
Pred. No. 0.00
43; Mismatches
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                                                                                                                                                                                                                                                                                          36;
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   208
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RESULT 7
NUIC PLEBO STANDARD; PRT; 372 AA.

ID NUIC PLEBO STANDARD; PRT; 372 AA.

AC Q00242;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-PEB-2003 (Rel. 41, Last annotation update)
DE NAD(P)H-quinone oxidoreductase chain 1 (EC 1.6.5.-) (NAD(P)
DE dehydrogenase 1, chain 1) (NDH-1, chain 1).

GN NDHA OR NDH1.
OS Plectonema boryanum.
OC Bacteria; Cyanobacteria; Oscillatoriales; Plectonema.
OX NCBI_TaxID=1184;
RN [1]
RP SEQUENCE FROM N.A.
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Matches 61
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SEQUENCE FROM N.A.
MEDLINE=99120557;
                                                                                                                                                                                                                        YH38 HAEIN
P44302;
01-NOV-1995
01-NOV-1995
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PFO:
TIGREAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
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                                                                                                                                                                                                                                                                                                                                          HAEIN
  SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
                                                                               Bacteria; Proteobacteria; Gammaproteobacteria;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                        Hypothetical
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                                                                                                                                                            Haemophilus
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th D.R., Noonan B., Guild B.C., deDonge B.L., Carmel G
mino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., I's
son R., Merberg D., Mills S.D., Jiang Q., Taylor D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ure 397:176-180(1999).
SUBCELULLAR IOCATION: Integral membrane protein
SIMILARITY: Belongs to the azlC family.
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Proj591; AzlC; 1.
AMS; TIGR00346; AzlC; 1.
hetical protein; Transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFRHVFYAFSFPLHVVKNPIARF-YSVFALIDEAYAVT---AARPAGWSAWRLISMQIAF 159
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14 34
42 6;
130 15
156 17
192 2;
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(Rel. 32, Last sequence update)
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protein HI1738.
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                                                                                                                                                                                                                                                                                                                      STANDARD;
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29.6%;
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Pred. No. 2.8e
11; Mismatches
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ROCCOGGGGGGGGG

Escherichia coli. Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

YGAZ ECOLI P76630; 15-JUL-1998 (R 15-JUL-1998 (R 16-OCT-2001 (R Hypothetical p

8 (Rel. 36, Created) 8 (Rel. 36, Last sequ 1 (Rel. 40, Last anno

sequence update) annotation updat

update)

STANDARD;

PRT;

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-i- SUBCELLULAR LOCATION: Integral membrane
-i- SIMILARITY: Belongs to the azlC family.
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| FFAMS; TIGR00346; AzlC; |
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57; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                             NFRHVFYAFS----FPLHVVKNPIARFYSVFALIDEAYA---VTAARPAGWSAWRLISMQ
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LVELLIIGKEYFLIPTLIGIWLILIMR
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                                                                                   FTIALVVIPGQALFAALLIFLGLLTIR
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7C61B72D4AF16021 CRC64;
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Pred. No. 4.3
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Max
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., R.
Mau B., Shao Y.;
                                                                                                                                     028519;
15-JUL-1998
15-JUL-1998
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997)
-i- SUBCELLULAR LOCATION: Integral membrane protein (Pote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.
STRAIN=K12 / MG1
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InterPro; IPR004471; AzlC.
Pfam; PF03591; AzlC; 1.
Hypothetical protein; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
  SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 4:
MEDLINE=98043943; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                       Archaea; Euryarchaeota;
Archaeoglobaceae; Archae
                                                                                                  Archaeoglobus fulgidus.
                                                                                                               AF1755.
                                                                                                                        Hypothetical
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25 4:
64 8:
110 13
141 1:
173 1:
206 2
245 AA;
                                                                                                                       (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation updat)
protein AF1755.
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                                                                                                                                                                                       STANDARD;
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lC family.
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RESULT 7
NUIC PLEBO STANDARD; PRT; 372 AA.

ID NUIC PLEBO STANDARD; PRT; 372 AA.

AC Q00242;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-PEB-2003 (Rel. 41, Last annoctation update)
DE MAD(P)H-quinone oxidoreductase chain 1 (EC 1.6.5.-
DE dehydrogenase I, chain 1) (NDH-1, chain 1).
GN NDHA OR NDH1.
OS Plectonema boryanum.
OC Bacteria; Cyanobacteria; Oscillatoriales; Plectone
NCBI_TaxID-1184;
RN [1]
RP SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the aziC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a control of the swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and to modified and this statement is not removed. Usage by and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
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14 34
37 55
123 14
155 17
189 20
219 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 E
57 E
143 E
175 E
209 WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.
; Transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
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POTENTIAL.
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265A2C88DA93EBB6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145;
No. 0.
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There are no restrictions
ong as its content is in
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es 96;
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Plectonema

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  RRAP OCCUPANTA
                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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Best Local S
Matches 61
                                                                                                                                                                                                                    P44302;
01-NOV-1995
01-NOV-1995
28-FEB-2003
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TRANSMEM
SEQUENCE
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TRANSMEM
TRANSMEM
TRANSMEM 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restue by non-profit institutions as long as its content use by non-profit institutions as long. It is content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-I- SUBCELIULAR LOCATION: Integral membrane protein (Potential).
-I- SIMILARITY: Belongs to the azlC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G. Tummino P.J., Caruso A., Uria.Nickelsen M., Mills D.M., I. Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
MEDLINE=99120557; PubMed=9923682;
MEDLINE=9120557; PubMed=9923682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trust
                                                                                                                                                                                                                                                                                                                              HAEIN
SEQUENCE FROM N.A. STRAIN=Rd / KW20 / MEDLINE=95350630; 1
                                                                                                         Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus,
                                                                                                                                                                                               Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001548; AAD06824.1; -. PIR; F71831; F71831.
                                                                                                                                                                                                                                                                                                           8 EHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAM8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF03591; AzlC; 1.
AMs; TIGR00346; azlC; 1.
hetical protein; Transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 NEKHVEYAESEPLHVVKNPIARE-YSVEALIDEAYAVT---AARPAGWSAWRLISMQIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPLGAIALTTLLV | | ; | ; | | ; ; ; | | ; ; ; | | ; ; ; | | ; ; ; | | ; ; ; | | ; ; ; | | ; ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; ; | ; | ; ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR004471; AzlC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 protein;
14 34
42 6;
130 15
156 17
192 21
228 AA;
                                                                                                                                                                             (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation updat
1 protein HI1738.
                                                                                                                                                          influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                           STANDARD;
    PubMed=7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 PC
62 PC
150 PC
176 PC
212 PC
25844 MW;
                         ATCC 51907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.1%;
                                                                                                                                   Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
SD6EBA86BE2E9744 CRC64;
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Pred. No. 2.8e
$1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                       223
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nes 95;
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                                                                                                                                     Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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۱, G. ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions on
tent is in no
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., Vovis G.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration -
MBL outstation -
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ROCCOGERRAN

Hypothetical property of B2682.

Enterobacteriaceae;
NCBI_TaxID=562;
[1]

Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Escherichia

976630; 15-JUL-1998 15-JUL-1998 16-OCT-2001

3 (Rel. 36, Created)
9 (Rel. 36, Last sequent (Rel. 40, Last annotation)
1 protein ygaz.

sequence update) annotation updat

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STANDARD;

PRT;

245

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RESULT
YGAZ_E
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Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004471; AzlC.

R Pfam; pF03591; AzlC; 1.

TIGRFAMS; TIGR00346; azlC; 1.

Hypothetical protein; Transmembrane; Complete proteome.

TRANSMEM 21 41

TRANSMEM 46 69 POTENTIAL.

TRANSMEM 66 86 POTENTIAL.

TRANSMEM 139 159 POTENTIAL.

TRANSMEM 139 159 POTENTIAL.

TRANSMEM 199 219 POTENTIAL.

TRANSMEM 199 219 POTENTIAL.

TRANSMEM 199 219 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fizzhugh W., Fields C.A., Gocayne J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Integral membrane
-!- SIMILARITY: Belongs to the azlC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole-genome random sequencing and assembly of {\tt Rd."}_i;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter J.
                                                                                                                              146
                                                                                                                                                                                                                            104
                                                                                                                                                            157
                                                                                                                                                                                             89
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5
                                                                                                                                                                                                                                                                                                                         57;
                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                          NFRHVFYAFS----FPLHVVKNPIARFYSVFALIDEAYA---VTAARPAGWSAWRLISMQ
                                                                                                                                                                                                                                                          GFLFLGIAYGIYKKALGFGFLYPTLMALLIYAGSVEFIAAGALIAPFSPI-SVLLITLMI
                                                             LVFLLIIGKEYFLIPTLIGIWLILTMR
                                                                                                                                                                                           GMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVI-ALVVGAAPLGAIALTTLLV
                                                                                               FTIALVVIPGQALFAALLIFLGLLTIR 242
                                                                                                                              LYLHIYWVLGAAMGNLFGTVLPFNLKGVEFSMTALFLVIFAENWLKGKSHESSLLGLGIA
                                                                                                                                                            IAFHSYWVFGGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDS-CRTKKQIPSLLLAGLS
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                         17.9%;
                                                                                                                                                                                                                                                                                                                         50;
                                                                                                                                                                                                                                                                                                                         Pred. No. 4.30); Mismatches
                                                                                                                                                                                                                                                                                                                                         Score 227.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                           4.3e-11;
                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                           87;
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                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                             13;
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                                                                                                                                                                                                                                                               88
                                                                                                                                                                215
                                                                                                                                                                                                                                                                                              103
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RESULT 1
AZLC_BACSU
ID AZLC_BAC
AC 007942;
          RX MEDLINE-98044033; PubMed=9384377;
RA KURST F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabrec C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Kasahara Y., Fuma S., Galizzi A., Galizron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Garandi G.,
RA Guiseppi G., Guy B.J., Haga X., Haiech J., Harwood C.R., Henaut A.,
RA Joris B., Karamata D., Kasahara Y., Klaerr Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue G.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue G.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S. H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Fortetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Robha E., Rabpoort G., Rey M., Reynolds S.,
RA Raber M., Sadaie Y., Schleich S., Schoeter R., Scoffone F.,
RA Sakiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
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MEDLINE=97453479; PubMed=9308178;
Sorokin A., Bolotin A., Purnelle B., Hilbert H.,
Sorokin A., Bolotin A., Ehrlich S.D.;
Duesterhoeft A., Ehrlich S.D.;
"Sequence of the Bacillus subtilis genome region
the lev operon reveals two new extracytoplasmic f
polymerase sigma factors SigV and SigZ.";
Microbiology 143:2939-2943(1997).
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MEDLINE=97431495; PubMed=9287000;
Belitsky B.R., Gustafsson M.C.U., Sonenshein A.L.,
"An lrp-like gene of Bacillus subtilis involved in
amino acid transport.";
J. Bacteriol. 179:5448-5457(1997).
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STRAIN=168;
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CLC3_RHUMAN
BDBC_FSERE
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protein search, using sw model

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Search time 13.9833 Seconds (without alignments) 934.659 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumetein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
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Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., Loftus B., Fizgerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., Fizgerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Godsyne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weldman J.M., Fujii C., Bowman C., Watthey L., Wallin E. Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
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Metical protein; Transport; Transmembrane; Complete proteome.

MEM 14 34 POTENTIAL.

MEM 42 62 POTENTIAL.

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                                                                                                                                                                                                                                                                                                                                                                                                                                    LGYLLMGMTFGMLLVQQGYDYKVALFMSLFIYAGAVQFVAITLLSAQASLMNVVIVSULV
                                                                                                                                                                                                                                             VVCL---ALFGTEYFLLIALVLMVLALMLFRK 224
                                                                                                                                                                                                                                                                                                       HSYWIFGSLVGSLVGSHFSFDTQGMEFVMTAIFIVLFMEQ---YKRTTNHKNAWLGIVIA
                                                                                                                                                                                                                                                                                                                                      HSYMVFGGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDSCRTKKQIPSLLLAGLSFTIA
                                                                                                                                                                                                                                                                                                                                                                        NAROTCYALSM-LDRFKNTKWRLPYLAHALTDETFALLNLYAPKEGVSEKDFIFSISLLN
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(Rel.
(Rel.
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                                              pylori J99 (Campylobacter pylori J99).
                                                                               protein JHP1251.
                                                                                                                                                              STANDARD;
                                                                                            40, Created)
40, Last seq
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                                Epsilonproteobacteria; Campylobacterales;
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                                                                                              sequence u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 235; DB 1;
Pred. No. 1.1e-11;
6; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE8EFAB6E8376130 CRC64;
                                                                                            update)
on update)
                                                                                                                                                              228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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MBL outstation -
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Search Job t	₽	Ş	뫄	₹	ďď	ş	рb	Ş
Search completed: April 16, 2004, 06:54:24 Job time : 21.5766 secs	Db 191 VLILAGTAALLNGLFSLFFPSGWSILLATLIASVGYEIGKAKK 233		Db 131 LTNGFVÍGVAVIAYVSMVVHSAVGYIVGSALÞATLQQGMGVÁLYAMÐIALLIÞSVRKHRS 190		Db 71 AIGTGTIEİLİTİFİVNİRHLLMSASIRAKMEDTHİVKRAITAFGITDEVFALVTSQDRR 130		Db 11 RETDWIRGAAIGSSIAIGYIPASITFGLLAKGTGITLIETIAMSIFVYAGASQYMALTLI 70	
			190	205	130	146	70	87

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A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11886360
A;Accession: AP0396
A;Status: preliminary
A;Molecule: Lype: DNA
A;Residues: 1-257 <KUR>
A;Residues: 1-257 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92498.1; PID:gl5981198; GSPDB:GN00: C;Genetics: A;Gene: YP03264
C;Superfamily: hypothetical protein b2682
                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, ; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunist A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 03-Jun-2002
C;Accession: H83390
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A;Experimental source: strain PAO1
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A; Residues: 1-252 <STO>
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Best Local S
Matches 52
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                                                                                                                                                                                                                                                                                                            Cross-references: GB:AL590842; PIDN:CAC92498.1; PID:g15981198; GSPDB:GN00175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNENRWYALGVGLTFYIAWNLFTLAGILLGRSIPGLEHLGLDFSIAATFIALVAPLVR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RQAFLRGAVAILPLSLAVAPWGLLAGSMAIEANLTPAEGQGLSAIVFAGAAQLVAIGMLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYEIAQGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVV 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAPEGAIALTTILIVNERHVEYAFSFPLHVVKNPIARFYSV---FALIDEAYAVTAARP- 144
  WVSALTVMAMDVRHILYG-
                                       GAIALTTLLVNFRHVFYAFSFPLHVVKNPIARFYS-----VFALIDEAYAVTAAR---
                                                                                                                        QGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGFFSIIFTTLLLTSQHLLYGMS--LRPVLSPLPGRWRIGLGFLLTDEFFALASQHDR 141
                                                                                 EGITDSLPIVIGYLPVAFAFGLSAVKLGFTPLESIFFSCIIYAGASQFVITALLSAGMSL
                                                                                                                                                                  Conservative
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                                                                                                                                                                13.8%; Score 175; DB 2;
25.8%; Pred. No. 1.3e-07;
tive 38; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47;
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  -PALKHRILAKLSGKKTALWAFGLTDEVFAAATTKLMK
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-235 <STO>
A;Cross-references: GB:AE005176; PID:g12724620; PIDN:AAK05711.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: E86826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid permease yqfD [imported] - Lactococcus lactis subsp. lactis (strain C;Species: Lactococcus lactis subsp. lactis
C;Dace: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: E86826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, Genome Res. 11, 731-753, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 -PAGWSAWRLISMQIAFHSYWVFGGLTGVAIA----ELIPFEIKGLEFALCSLFVTLTLD 198
177 LYLQLISDKTLGLMLQLVMVGITLVLFYFGLIFLPSNLLVLFVTLIACALGVGVKRVFF
                                                                                                                                                 140 ----TAARPAGWSAWRLISMQIAFHSYWVFGGLTGVAIAELIPFEIKGLEFALCSLFV-- 193
                                                                                                                                                                                                          69
                                                                                                                                                                                                                                                         94 GAIALTTLLUNFRHVFYAFSFPLHVVKNPIARFYSVFALI-DEAYAV-------
                                                                                                                                                                                                                                                                                                                                                              34 QGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPL
                                                                                                                                                                                                                                                                                                             ø
                                                                                                                                                                                                       MSIVLSVFLVNSRIILMSMTTASYFKNESILKNILLGTÜLTDESFÄLGMNKONYTEGKLN 128
                                                                                                                                                                                                                                                                                                             QGLKDTMPTVFGYIGIGIAFGMIGHSEGFSVWVILLLSLIVYAGSAQFIMVSMLATHSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S--FKROYSLTVIÁSLSGALLGVLLFSIPVAILAGIA 229
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                                              -TLTLDSCRTKKQIPSLLLAGLS---FTIALVVIPGQ--ALFAALL-IFLGLLTIRVFF 245
                                                                                                  PSWFNASNLLAYLVWALAS------AIGALLGNLLAN--P-EXLGLGFAVIAMFIGL 176
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            13.8%; Score 174.5; DB 2; 25.5%; Pred. No. 1.3e-07; ative 47; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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F84013

branched-chain amino acid transporter BH2910 [imported] - Bacillus halodurans (strain C;Species: Bacillus halodurans C;Species: Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 01-Mar-2002 C;Accession: F84013 R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Hi Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans an A;Reference number: A83650; MUID:20512582; PMID:11058132 A;Accession: F84013

and

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A;Status: preliminary

A;Molecule type: DNA A;Residues: 1-237 <STO> A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB06629.1; GSPDB:GN00 A;Experimental source: strain C-125

Superfamily: hypothetical protein b2682;

Genetics:

Query Match Matches Local Similarity 55; Conserv Conservative 13.8%; Score 174.5; DB 2 23.7%; Pred. No. 1.3e-07; 48; Mismatches DB 2; Length 237; 17;

6

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R;Goodner, B; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: B97492

A;Status: preliminary
A;Across-references: GB:AE007869; PIDN:AAX86891.1; PID:g15156113; GSPDB:GN00169

C;Genetics:
AZIC family protein VCA1002 [imported] - Vibrio cholerae (strain N16961 serogroup)
C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Accession: G82388
R;Heidelberg, J.F; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, Chardson, D.; Ermolaeva, M.D.; Vennathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sell.
R.R.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20408833; PMID:10952301
A;Accession: G82388
A;Astus: preliminary
A;Molecule type: DNA
A;Residues: 1-239 <HEI>A;Cross-references: GB:AE004427; GB:AE003853; NID:99658442; PIDN:AAF96898.1; GSPDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            azlC family protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon) C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: B97492 C;Accession: B97492 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.;
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;Superfamily: hypothetical protein b2682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGAAPLGAIALTTILIVNERHVEYAFSEPLHVVKNPIA------RFYSVFALIDEAY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIVLLMGFWKGRETGLVLLASASAACLTHALVPGAWYIAA 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRYEIAQGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALABERVIAGRUTAAFFAGAALSIYLVWNLATLAGALLGAVVGDM---SVIĞLDFAFPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVTAAR-----PAGWSAWRLISMQIAFHSYWVFGGLTGVAIAELIPFEIKGLEFALCSL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIVILMGFWKGRETGLVILASASAACLTHALVPGAWYIAA
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; Pred. No. 3.6e-08;
46; Mismatches 91
               GB:AE003853; NID:g9658442; PIDN:AAF96898.1; GSPDB:GN001
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I.; Sellers,
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RESULT 12 H83390

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168

MORRIPVRNLLILAVVAVSFFLLLTVMSQSLAVLFATLL

207

hypothetical

protein PA2039

[imported]

Pseudomonas

aeruginosa

(strain

PAO1)

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A;Experimental source: serogroup O1; strain N16961; biotype E1 C;Genetics:
A;Gene: VCA1002
A;Map position: 2
C;Superfamily: hypothetical protein b2682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein SP0146 [imported] - Streptococcus pneumoniae (strain TIGE C,Species: Streptococcus pneumoniae
C,Species: Streptococcus pneumoniae
C,Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C,Daccession: G95016
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A;Accession: G95016
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A;Experimental source: strain TIGR4
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A; Residues: 1-218 < KUR>
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Best Local S
Matches 63
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                                                                                                                                             ---WSAWRLISMQIAFHSYWVFGGLTGVAIAELIPF-EIKGLEFALCSLFVTLTLDSCR- 201
                                                                                                                                                                                                                                                                                                                                                                                                                            TAAGLGMYPIGIAFGLLVIQYGYBWWAAPLFSGL----IFAGSTEMLVIALVVGAAPLGA
           TKKQIP-----SLLLAGLSFTIALVVIPGQ--ALFAALL
                                                                                     NPMWMHGNNLNSYVA--
                                                                                                                                                                                                                    IAMTVFLINLR----LFLLSLHASTYFRHTSLWYNIGMSSILTDETYGVLMGELAHTDKV 111
                                                                                                                                                                                                                                                                                       IALTTLLVNFRHVFYAFSFPLHVVK--NPIARFYSV---FALIDBAYAVTAARPAG---- 146
                                                                                                                                                                                                                                                                                                                                                                 MPTALGYVSIGLACGIIGAPY-----VTPVEMGLMSLFVYAGSAQFAMLALIVVQAPVAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.0%; Score 177.5; DB 2; larity 28.6%; Pred. No. 6.7e-08; Conservative 36; Mismatches 82;
                                                                                         --WFVGTVVGTALGGĹLÞNÞĖÍFGLDFALVGMFIGIFASQFQI 167
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A;Gene:
C;Superf
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A;Residues: 1-245 <STO>
A;Cross-references: GB:AE005174; NID:g12517123; PIDN:AAG57791.1; GSPDB:GN00145;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A85480;
A;Accession: C85916
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 8, 11-22, 2001
A,Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A,Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H91071
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A,Residues: 1-245 <HAY>
A,Cross-references: GB:BA000007; PIDN:BAB36967.1; PID:g13363015;
A,Experimental source: strain O157:H7, substrain RIMD 0509952
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A;Molecule type: DNA
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Best Local S
Matches 68
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                                                                                                                                                                                                                                      34 QGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68;
                                                                                                                                                                                                                                                                          68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                    WVAALTVMAMDVRHVLYGPSLRSRIIQRLQKSKTALW--AFGLTDEVFAAATAKLVRNNR 134
                                                                                                                                                                     GAIALTILLVNFRHVFYAFSFPLHVV----KNPIARFYSVFALIDEAYAVTAAR----PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKQ-----SLCVTAALVGALAGVTLFSIPVAILAGIVCGCLTALIQAFWQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKKQIPSILLAGI.SFTIALV-VIPGQALFA---ALL--IFLGLLT--IRYFFIG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RWSENWMIGIAFSSWSSWVFGTVIGAFSGSGLLQGYPAVEAALGFMLPALFMSFLLASFQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GWSAWRLISMQIAFHSYWVF----GGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDSCR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WVAALTVMAMDVRHVLYGPSLRSRIIQRLQKSKTALW--AFGLTDEVFAAATAKLVRNNR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAIALTILLVNFRHVFYAFSFPLHVV----KNPIARFYSVFALIDEAYAVTAAR----PA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGCKDSLPIVISYIPVAFAFGLNATRIGFSPLESVFFSCIIYAGASQFVITAMLAAGSSL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPL
                                TKKQIPSLLLAGLSFTIALV-VIPGQALFA---ALL--IFLGLLT--IRYFFLG 247
                                                                   RWSENWMIGIAFSSWSSWVFGTVIGAFSGSGLLQGYPAVEAALGFMLPALFMSFLLASFQ
                                                                                                  GWSAWRLISMQIAFHSYWVF----GGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDSCR 201
                                                                                                                                                                                                       EGCKDSLPIVISYIPVAFAFGLNATRLGFSPLESVFFSCIIYAGASQFVITAMLAAGSSL
RKO--
                                                                                                                                                                                                                                                                                                                                          hypothetical protein b2682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han,
Kasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.6%; Score 198; DB 2; ilarity 29.1%; Pred. No. 1.4e-09; Conservative 41; Mismatches 95
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                     15.6%;
   -SLCVTAALVGALAGVTLFSIPVAILAGIVCGCLTALIQAFWQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                         41; Mismatches
                                                                                                                                                                                                                                                                                         Score 198; DB 2; Length 245; Pred. No. 1.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                                                                 GSPDB:GN00154
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hypothetical protein b2682 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
C;Accession: C65048
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; I
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C65048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE000353; GB:U00096; NID:g1789037; A;Experimental source: strain K-12, substrain MG1655 C;Superfamily: hypothetical protein b2682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-245 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
  195
                                                           202
                                                                                                              135
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                                                                                                                                                                                                                            77 WIAALTVWAMDVRHVLYGPSLRSRIIQRLQKSKTALW--AFGLTDEVFAAATAKLVRNNR 134
                                                                                                                                                                                                                                                                         94 GAIALTTLLVNERHVEYAFSFPLHVV----KNPIAREYSVFALIDEAYAVTAAR----PA 145
                                                                                                                                                                                                                                                                                                                                          17
                                                                                                                                                                                                                                                                                                                                                                                             34 QGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALVVGAAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                             GWSAWRLISMQIAFHSYWYF----GGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDSCR 201
                                                                                                                                                                                                                                                                                                                                    TKKQIPSILLAGLSFTIALV-VIPGQALFA---ALL--IFLGLLT--IRYFFIG 247
                                                                                                              RWSENWMIGIAFSSWSSWVFGTVIGAFSGSGLLQGYPAVEAALGFMLPALFMSFLLASFQ
RKQ-----SICVTAALVGALAGVTLFSIFVAILAGIVCGCLTALIQAFWQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.5%; Score 197; DB 1; Length 245; 29.1%; Pred. No. 1.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN:AAC75729.1; PID:g1789038;
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                                                                                                                       194
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branched-chain amino acid permease Atu1082 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: A12709
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Merage, G.; Gillet, W.; Grang, S.
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-3323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-

A;Cross-references: GB:AE008688; PIDN:AAL42095.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics: A;Status: preliminary A;Molecule type: DNA A;Residues: 1-234 <KUR> ster, E.W. A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58 A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Accession: AI2709 PID:g17739477; GSPDB:GN00186

W.; Perry, M.; Gordon-Kamm

, Woo, I
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A;Gene: Atu1082
A;Map position: circular chromosome C;Superfamily: hypothetical protein **b2682**

밁 Matches Query Match Local Similarity es 55; Conserv თ RRYETAQGLKTSLAAGLGMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVIALV KRAELIAGLRSAAPLLVAMVPIGVVFGAVAIGKGLSPLEASLMSLLVFAGGSQFVAMDLW Conservative 14.3%; 46; Score 181; DB 2; Pred. No. 3.6e-08; 6; Mismatches 91; Length Indels Gaps <u>ი</u> 87

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conserved hypothetical integral membrane protein HP1331 - Helicobacter pylori (Stra C.)Species: Helicobacter pylori (C.)Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jun-2000 C.Accession: C64686 R.Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; Mc1 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Frijii, C.; Bowman, C.; Watthey Nature 388, 539-547, 1997
A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Frase; A.; Reference number: A64520; MUID:97394467; PMID:9252185
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                                                                                                                                                                C;Accession: F71831

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, (Nature 397, 176-180, 1999

Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastri A;Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: F71831
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F71831
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                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-228 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                               ypothetical protein jhp1251 - Helicobacter pylori (strain J99)
;Species: Helicobacter pylori
;Variety: strain J99
;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:AE000634; GB:AE000511; NID:g2314489; PIDN:AAD08372.1; Superfamily: hypothetical protein b2682
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:Residues: 1-228 <T\
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                                                             Cross-references: GB:AE001548; Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::: | | : |:| ||:||:
LILFGGNQFIIPAMLAILGVLTV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVIPG--OALFAALLIFLGLLTI 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYWVFGGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDSCRTKKQIPSLLLAGLSFTIAL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NARHLFYGISMLDKYRGTGKKKLYLIFGMCDESFSINYTANVPANVDKGWFMFFVTLLNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NARQTCVALSM-LDRFKNTKWRLPYLAHALTDETFALLNLYAPKEGVSEKDFIFSISLLN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFRHVFYAFSFPLHVVKNPIARF-YSVFALIDEAYAV--TAARPAGWSAWRLI-SMQIAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSYWIFGSLVGSLVGSHFSFDTQGMEFVMTAIFIVLFMEQ---YKRTTNHKNAWLGIVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSYWVFGGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDSCRTKKQIPSLLLAGLSFTIA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGYLLMGMTFGMLLVQQGYDYKVALFMSLF1YAGAVQFVA1TLLSAQASLMNVVIVSLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVCL---ALFGTEYFLLIALVLMVLALMLFRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVVIPGOALFAA---LLIFLGLLTIRYFFLGK 248
hypothetical
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  protein b2682
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Pred. No. 9.2e-
36; Mismatches
                                                                                   GB:AE001439;
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).2e-13;
1es 92;
                                                                                   NID:g4155845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224
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                                                                                        PIDN:AAD06824.1;
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                                                                                     PID:g415589
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hypothetical protein HI1738 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
C;Accession: F64041
C;Accession: F64041
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, Gocayne, J.D.; Frine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: F64041
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A; Residues: 1-244 < TIGR>
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Best Local S
Matches 61
                                                                                Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                            Cross-references: GB:U32846; GB:L42023; NID:g3212237;
Superfamily: hypothetical protein b2682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGYLLMGMTFGMLLAQQGYDYKVALFMSLFIYAGAIQFVAITLLSAQASLMNVVIVSLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSYMIFGSLVGSLVGSHFSFDTQGMEFVMTAIFIVLFMEQYKRNTNHKNAWL-GIAIAVV
GFLFLGIAYGIYMKALGFGFLYPTLMALLIYAGSVEFIAAGALIAFFSPI-SVLLITLMI
                                         GMYPIGIAFGLLVIQYGYEWWAAPLFSGLIFAGSTEMLVI-ALVVGAAPLGAIALTTLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                  Conservative
                                                                                      17.9%;
27.5%;
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29.6%; Pred. No. 2.7e-
tive 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
                                                                                  50;
                                                                              Score 227.5; DB 1
Pred. No. 4.3e-12;
0; Mismatches 87
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hypothetical protein 23983 [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli (c;Species: Escherichia coli (c;Species: Escherichia coli (c;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 01-Mar-200 C;Accession: C85916 [Strain of C, Mariand, V.; Mau, B.; Glasner, J.D.; Rose R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis Nature 409, 529-533, 2001 [Nature 409, 529-533, 2001]
                                                                                                                                                                                                                                             RESULT
C85916
                                                                    J.D.; Rose,
Potamousis,
                                                                                                                                                                  01-Mar-2002
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LYLHIYWVLGAAMGNLFGTVLFFNLKGVEFSMTALFLVIFAENWLKGKSHESSLLGLGIA IAFHSYWVFGGLTGVAIAELIPFEIKGLEFALCSLFVTLTLDS-CRTKKQIPSLLLAGLS 215 SARQIFYGISMLEKYGIHIGKK----RWYLITTLVDESFSLNYMAKIPPHLDKGWYMFFVS

205

145

242

89

30

104 NFRHVFYAFS----FPLHVVKNPIARFYSVFALIDEAYA---VTAARPAGWSAWRLISMQ 156

S

LVFLLIIGKEYFLIPTLIGIWLILTMR FTIALVVIPGQALFAALLIFLGLLTIR

	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - pro	protein search, using sw model
Run on:	April 16, 2004, 06:51:17; Search time 19.5766 Seconds (without alignments) 1233.313 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-608-504-3 1269 1 MOXTOEIHSSLEVSPSKAALLLIFLGLLTIRYFFLGKAAK 251
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	283366 seqs, 96191526 residues
Total number of	Total number of hits satisfying chosen parameters: 283366
Minimum DB seq l Maximum DB seq l	seq length: 0 seq length: 2000000000
Post-processing: Minimum Match Maximum Match Listing first	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	PIR 78:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*
Pred. No.	is the number of results predicted by chance to have a

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22					17	16	15	14	13	12	11	10	9	89	7	თ	U				1		Result No.
112	112	113.5	115	137	140	140.5	145	145.5	145.5	147	163.5	166	169	174.5	174.5	175	175	177.5	181	181	181	197	198	198	227.5	229.5	235	240		Score
8.8	8.8		٠	10.8		11.1	11.4	٠	11.5	11.6	12.9	'n	ω.	ω	13.8			14.0	•	14.3	4	'n		15.6	٠	٠	18.5	18.9		Query
490	379	477	140	235	160	246	219	240	240	231	219	235	235	237	235	257	252	218	239	234	234	245	245	245	244	228	228	254		Length
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ALIGNMENTS

Oy 104 NERHVEYAFSEPLHVVKNPIARFYS	Oy 45 GMYPIGIAFGLLVIQYGYEWWAAPI : : : : Db: 42 GFLFLGIAYGIFMHSLGFSAIYPII	Query Match Best Local Similarity 30.5%; Pred, Matches 62; Conservative 44; Mi	A;Status: translated from GB/RMBL/DDBJ A;Molecule type; DNA A;Residues: 1-254 <bel> A;Cross-references: EMBL:Y11043; NID:g1926275; PIDN:CAA71940.1; A;Experimental source: strain 1A1 C;GenetLcs: A;Gene: azlC C;Superfamily: hypothetical protein b2682</bel>	R;Belitsky, B.R.; Gustafsson, M.C.U.; Sonenshein, A.L.; J. Bacteriol. 179, 5448-5457, 1997 A;Title: An Irp-like gene of Bacillus subtilis involved A;Reference number: Z22837; MUID:97431495; PMID:9287000 A;Accession: T44777	A;Status: nucleic acid sequence not shown; translation not A;Molecule type: DNA A;Hesidus: 1-254 cKUNs A;Cross-references: GB:Z99117; GB:AL009126; NID:g2634966; A;Experimental source: strain 168	A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, iech, J; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsa Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Ku A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; S. akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; T.; Winters, P.; Mipat, A.; Yamamoto, H.; Yamane, K.; Y. A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H. A;Title: The complete genome sequence of the Gram-posit A;Reference number: A69580; MUID:98044033; PMID:9384377 A;Accession: G69592	RESULT 1 G69992 branched-chain amino acid transport azlC C.Species: Bacillus subtilis C.Date: 10-Sep-1999 #sequence_revision 10 C;Accession: G69592; T44777 R;Kunst, F.; Ogasawara, N.; Moszer, I.; J C.; Bron, S.; Brouillet, S.; Bruschi, C.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian Nature 190, 240-256 1997
104 NERHVEYAESEPLHVVKNPIAREYSVEALIDEAYAVTAARPAGW-SAWRLISNGIAEH 160	GNYPIGIAFGLLVIQYGYEWWAAPLESGLIFAGSTEMLVIALVVGA-APLGAIALTILLV 103 : : : :	Score 240; DB 1; Length 254; Pred. No. 3.9e-13; ; Mismatches 89; Indels 8; Gaps 6;	91926275; PIDN:CAA71940.1; PID:g1926281 2682	Sonenshein, A.L.; von Wachenfeldt, C. subtilis involved in branched-chain amino acid tral495; PMID:9287000	A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-254 <kun> A;Cross-references: GB:Z99117; GB:AL009126; NID:g2634966; PIDN:CAB14612.1; PID:g2635116 A:Experimental source: strain 168</kun>	A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A., Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serox akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A; Leit, E.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Reference number: A69580; MUID:98044033; PMID:9384377	RESULT 1 G69592 branched-chain amino acid transport azlC - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 C;Accession: G69592; T44777 C;Accession: G69592; T44777 R;Kunst, F; Ogasawara, N; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc C.; Brilich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B. Nature 1400 249-56 1907